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OM protein - protein search, using sw model

Run on: February 16, 2006, 18:26:01 ; Search time 188 Seconds  
(without alignments)  
137.890 Million cell updates/sec

Title: US-10-021-963-2

Perfect score: 358

Sequence: 1 GPGDACLPAVQGFRCRGP.....EGNNFHSRSCDACPVP 59

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	358	100.0	59	3	Aay84381 Amino aci
2	358	100.0	59	5	Aau79237 Human Kun
3	358	100.0	59	6	Abg72330 Human Kun
4	358	100.0	408	8	Adr09156 Human pro
5	358	100.0	491	8	Abc00003 Human gen
6	358	100.0	548	4	Aab83435 Human zku
7	358	100.0	548	4	Aag65899 Amino aci
8	358	100.0	548	6	Abg74120 Human pro
9	358	100.0	548	7	Aae39463 Human GDF
10	358	100.0	548	7	Adp93678 Human GDF
11	358	100.0	548	9	Aea22339 Human GAS
12	323	90.2	552	7	Aae39462 Mouse GDF
13	323	90.2	552	7	Adp93676 Mouse GDF
14	323	90.2	552	9	Aea22337 Mouse GAS
15	239	66.8	283	8	Adg36986 Kunitz ty
16	239	66.8	503	5	Abj01150 Ovary cel
17	239	66.8	549	8	Adj66077 Rat prote
18	239	66.8	576	4	Aab82874 Human Kun
19	239	66.8	576	5	Aau74559 Human zku
20	239	66.8	576	6	Ada01258 Human zku
21	239	66.8	576	7	Aae39461 Human GDF
22	239	66.8	576	7	Adp93674 Human GDF
23	239	66.8	576	8	Adg36984 Human Kun
24	239	66.8	576	8	Adj66073 Rat prote

25	239	66.8	576	8	ADJ66075	Adj66075 Rat prote
26	239	66.8	576	8	ADR09500	Adr09500 Human pro
27	239	66.8	576	9	AEA22335	Aea22335 Human GAS
28	239	66.8	640	7	AAE39460	Aae39460 Human GDF
29	239	66.8	640	7	ADD93672	Add93672 Human GDF
30	239	66.8	640	9	AEA22333	Aea22333 Human GAS
31	227	63.4	571	7	AAE39498	Aae39498 Cloned mo
32	227	63.4	571	7	AAE39459	Aae39459 Mouse GDF
33	227	63.4	571	7	ADD93670	Add93670 Mouse GDF
34	227	63.4	571	7	AEA42236	Aea42236 Mouse GDF
35	227	63.4	571	9	AEA22377	Aea22377 Mouse GAS
36	227	63.4	571	9	AEA22331	Aea22331 Mouse GAS
37	178	49.7	655	7	ADP42044	Adp42044 C-termina
38	178	49.7	655	8	ADR90036	Adr90036 C-termina
39	178	49.7	728	7	ADF42058	Adf42058 Albumin f
40	178	49.7	728	8	ADR90050	Adr90050 Mature pD
41	178	49.7	729	8	ADF42029	Adf42029 DPI-14-(G
42	178	49.7	729	8	ADR90021	Adr90021 Mature pD
43	178	49.7	752	7	ADP42057	Adp42057 Plasmid p
44	178	49.7	752	8	ADR90049	Adr90049 pDB300X3
45	178	49.7	753	7	ADF42028	Adf42028 DPI-14-(G

ALIGNMENTS

RESULT 1  
AAY84381  
ID AAY84381 standard; protein; 59 AA.  
XX  
AC AAY84381;  
XX  
DT 12-JUL-2000 (first entry)  
XX  
DE Amino acid sequence o a serine proteinase inhibitor designated ZKUN6.  
XX  
KW Serine proteinase inhibitor; kunitz domain; ZKUN6; acute pancreatitis;  
KW cardiopulmonary bypass-induced pulmonary injury; myocardial infarction;  
KW allergy-induced protease release; deep vein thrombosis; shock;  
KW hyperfibrinolytic haemorrhage; emphysema; rheumatoid arthritis;  
KW adult respiratory distress syndrome; chronic inflammatory bowel disease;  
KW psoriasis; inflammatory conditions; platelet function; fibrinolysis;  
KW organ preservation; wound healing; haemostasis imbalance; cirrhosis;  
KW acquired coagulopathy; primary fibrinolysis; thrombolytic therapy;  
KW blood coagulation; proteolytic tissue degradation; gene therapy.  
XX  
OS Homo sapiens.

XX	Key	Location/Qualifiers
FT	Disulfide-bond	6..56
FT	Domain	14..20
FT	Disulfide-bond	15..39
FT	Disulfide-bond	31..52
XX	WO200014235-A1.	
XX	16-MAR-2000.	
XX	01-SEP-1999;	99WO-US020202.
XX	03-SEP-1998;	98US-00148092.
XX	(ZYMO ) ZYMOGENETICS INC.	
XX	Conklin DC;	
XX	WPI; 2000-256985/22.	
XX	N-PSDB; AAZ99802, AAZ99803.	
XX	Novel proteinase inhibitor Zkun6 comprising a kunitz domain, useful in the treatment or prevention of conditions associated with excessive proteinase activity.	

XX \*  
 PS Claim 4; Page 40; 48pp; English.  
 XX  
 CC The present sequence represents a serine proteinase inhibitor containing  
 CC a kunitz domain, designated ZKUN6. The zkun6 polypeptides are used in the  
 CC treatment and prevention of conditions associated with excessive  
 CC proteinase activity. The conditions include acute pancreatitis,  
 CC cardiopulmonary bypass-induced pulmonary injury, allergy-induced  
 CC protease release, deep vein thrombosis, myocardial infarction, shock,  
 CC hyperfibrinolytic haemorrhage, emphysema, rheumatoid arthritis, adult  
 CC psoriasis, inflammatory conditions, chronic inflammatory bowel disease,  
 CC conditions arising from haemostasis imbalance, including acquired  
 CC coagulopathies, primary fibrinolysis and fibrinolysis due to cirrhosis,  
 CC and complications of high-dose thrombolytic therapy. Zkun6 polypeptides  
 CC may also be used for inhibiting blood coagulation in mammals, and for  
 CC blockage of proteolytic tissue degradation. The zkun6 polynucleotides are  
 CC used in gene therapy to treat the above diseases. Transgenic animals,  
 CC engineered to express zkun6, and knockout animals with an absence of  
 CC zkun6 function, are used to study the zkun6 gene and the encoded protein.  
 CC They are useful for investigating the role of zkun6 polypeptides in early  
 CC development  
 XX  
 SQ Sequence 59 AA;

Query Match 100.0%; Score 358; DB 3; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-34;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGDACVLPAVQGPCRGWEPRWAYSPLLQQCHPFFVYGCCEGNNFHSRSCEDACPVP 59  
 Db 1 GPGDACVLPAVQGPCRGWEPRWAYSPLLQQCHPFFVYGCCEGNNFHSRSCEDACPVP 59

RESULT 2  
 AAU79237  
 ID AAU79237 standard; protein; 59 AA.  
 XX  
 AC AAU79237;

XX  
 XX 30-JUL-2002 (first entry)  
 DT  
 DE Human Kunitz inhibitor protein (zkun6).  
 XX

XX Human; zkun6; serine proteinase; Kunitz inhibitor protein; trypsin;  
 KW plasmin; kallikrein; elastase; cathepsin G; proteinase-3; shock;  
 KW thrombin; factor VIIa; factor IXa; factor Xa; factor XIIa; factor XIIIa;  
 KW matrix metalloproteinase; acute pancreatitis; deep vein thrombosis;  
 KW cardiopulmonary bypass-induced pulmonary injury; myocardial infarction;  
 KW allergy-induced protease release; hyperfibrinolytic haemorrhage;  
 KW emphysema; rheumatoid arthritis; adult respiratory distress syndrome;  
 KW chronic inflammatory bowel disease; psoriasis; inflammatory condition;  
 KW platelet function; organ preservation; wound healing; haemostasis;  
 KW acquired coagulopathy; fibrinolysis; cirrhosis; liver disease; uraemia.  
 XX

OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 6..56  
 FT /label= Kunitz domain  
 FT /note= "This region is specifically claimed"

XX  
 FN USG380354-B1.  
 XX  
 XX 30-APR-2002.  
 PD  
 XX  
 XX 01-SEP-1999; 99US-00388183.  
 PF  
 XX  
 XX 03-SEP-1998; 99US-0099296P.  
 PR  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 PA  
 XX

PI Conklin DC;  
 XX  
 DR WPI; 2002-413725/44.  
 DR N-PSDB; ABK50403.  
 XX  
 PT Isolated serine proteinase Kunitz Inhibitor Protein zkun6, useful for  
 PT treating e.g. inflammatory bowel disease, psoriasis, and other  
 PT inflammatory conditions.  
 XX  
 XX Claim 4; Page 2; 18pp; English.

XX The invention relates to an isolated serine proteinase Kunitz inhibitor  
 CC protein, zkun6 and the polynucleotide encoding it. The zkun6 protein is  
 CC useful in the treatment or prevention of conditions associated with  
 CC excessive proteinase activity, in particular an excess of trypsin,  
 CC plasmin, kallikrein, elastase, cathepsin G, proteinase-3, thrombin,  
 CC factor VIIa, factor IXa, factor Xa, factor XIIa, factor XIIIa, or matrix  
 CC metalloproteinases. Such conditions include acute pancreatitis,  
 CC cardiopulmonary bypass (CPB)-induced pulmonary injury, allergy-induced  
 CC protease release, deep vein thrombosis, myocardial infarction, shock  
 CC (including septic shock), hyperfibrinolytic haemorrhage, emphysema,  
 CC rheumatoid arthritis, adult respiratory distress syndrome, chronic  
 CC inflammatory bowel disease, psoriasis, and other inflammatory conditions.  
 CC Zkun6 proteins are also used in preservation of platelet function, organ  
 CC preservation and wound healing. Zkun6 proteins may be useful in the  
 CC treatment of conditions arising from an imbalance in haemostasis,  
 CC including acquired coagulopathies, primary fibrinolysis and fibrinolysis  
 CC due to cirrhosis, and complications from high-dose thrombolytic therapy.  
 CC Acquired coagulopathies can result from liver disease, uraemia, acute  
 CC disseminated intravascular coagulation, post-cardiopulmonary bypass,  
 CC massive transfusion or warfarin overdose. This sequence represents the  
 CC human zkun6 protein of the invention  
 XX  
 SQ Sequence 59 AA;

Query Match 100.0%; Score 358; DB 5; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-34;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGDACVLPAVQGPCRGWEPRWAYSPLLQQCHPFFVYGCCEGNNFHSRSCEDACPVP 59  
 Db 1 GPGDACVLPAVQGPCRGWEPRWAYSPLLQQCHPFFVYGCCEGNNFHSRSCEDACPVP 59

RESULT 3  
 ABG72330  
 ID ABG72330 standard; protein; 59 AA.  
 XX  
 AC ABG72330;  
 XX  
 DT 30-JAN-2003 (first entry)  
 XX  
 DE Human Kunitz domain protein zkun6.  
 XX  
 XX Human; zkun6; excessive proteinase activity; anticoagulant;  
 KW acute pancreatitis; cardiopulmonary bypass-induced pulmonary injury;  
 KW allergy-induced protease release; deep vein thrombosis;  
 KW myocardial infarction; shock; hyperfibrinolytic haemorrhage; emphysema;  
 KW rheumatoid arthritis; adult respiratory distress syndrome;  
 KW chronic inflammatory bowel disease; psoriasis; inflammatory condition;  
 KW platelet preservation; organ function; wound healing;  
 KW proteolytic tissue degradation; kunitz domain.  
 XX

OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 6..56  
 FT /note= "This region is specifically claimed in"  
 XX  
 XX US2002110887-A1.  
 FN  
 XX 15-AUG-2002.  
 XX

PF 14-DEC-2001; 2001US-00021963.  
 XX  
 PR 03-SEP-1998; 98US-009296P.  
 PR 01-SEP-1999; 99US-00388183.  
 XX  
 PA (ZYMO) ZYMOGENETICS INC.  
 XX  
 PI Conklin DC;  
 XX  
 DR WPI; 2003-066687/06.  
 DR N-PSDB; ABS57116.  
 XX  
 XX New proteinase inhibitor, zkm6, useful for treating or preventing  
 PT conditions associated with excessive proteinase activity, e.g. chronic  
 PT inflammatory bowel disease, psoriasis, hyperfibrinolytic hemorrhage or  
 PT emphysema.  
 XX  
 PS Claim 1; Fig 1; 19pp; English.  
 XX  
 CC The invention relates to an isolated protein comprising residues 6-56 of  
 CC the human kunitz domain protein zkm6 appearing as ABG72330, or a protein  
 CC 80% identical to it. Also included are: (1) an expression vector  
 CC comprising the following operably linked elements: (a) a transcription  
 CC promoter; (b) a DNA segment encoding a protein of 51-81 amino acid  
 CC residues of zkm6; and (c) a transcription terminator; (2) a cultured  
 CC cell containing the expression vector, where the cell expresses the DNA  
 CC segment; (3) making a protein by culturing the cell; and (4) an antibody  
 CC that specifically binds to the zkm6 segment. The zkm6 proteins are  
 CC useful for treating or preventing conditions associated with excessive  
 CC proteinase activity (e.g. acute pancreatitis, cardiopulmonary bypass-  
 CC induced pulmonary injury, allergy-induced protease release, deep vein  
 CC thrombosis, myocardial infarction, shock, hyperfibrinolytic haemorrhage,  
 CC emphysema, rheumatoid arthritis, adult respiratory distress syndrome,  
 CC chronic inflammatory bowel disease, psoriasis and other inflammatory  
 CC conditions). The proteins may also be used in preserving platelet and  
 CC organ function, and wound healing, for inhibiting blood coagulation in  
 CC mammals, in blockage of proteolytic tissue degradation and in preparing  
 CC antibodies that specifically bind to zkm6 proteins. The present sequence  
 CC represents zkm6  
 XX  
 SQ Sequence 59 AA;  
 Query Match 100.0%; Score 358; DB 6; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-34;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GPGDACLPAVQGPCRGWEPRWAYSPLLQQCHPFFVYGGCEGNNFHRSCEADACPVP 59  
 |||||  
 Db 1 GPGDACLPAVQGPCRGWEPRWAYSPLLQQCHPFFVYGGCEGNNFHRSCEADACPVP 59  
 |||||  
 RESULT 4  
 ADRO9156  
 ID ADRO9156 standard; protein; 408 AA.  
 XX  
 AC ADRO9156;  
 XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 DE Human protein useful for treating neurological disease Seq 2662.  
 XX  
 KW human; oligo-capping method; diagnostic marker; gene therapy;  
 KW osteoporosis; neurological disease; Alzheimer's disease;  
 KW Parkinson's disease; dementia; short memory; cancer;  
 KW sense or motor function; emotional reaction; fear response; panic;  
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
 KW tranquiliser.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EPI447413-A2.  
 XX  
 XX EPI447413-A2.  
 PD 18-AUG-2004.  
 XX

XX 12-FEB-2004; 2004EP-00003145.  
 XX  
 PR 14-FEB-2003; 2003JP-00102207.  
 PR 09-MAY-2003; 2003JP-00131452.  
 XX  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;  
 PI Wakamatsu A, Ishii S, Nagai K, Irie R;  
 XX  
 DR WPI; 2004-583265/57.  
 DR N-PSDB; ADR07200.  
 XX  
 XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,  
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
 XX  
 PS Claim 1; SEQ ID NO 2662; 2686pp; English.  
 XX  
 CC This invention relates to novel, isolated full length human cDNA  
 CC molecules and the encoded proteins thereof. Specifically, it refers to  
 CC cDNA clones obtained by an oligo-capping method, where none of these  
 CC clones are identical to any known human mRNAs. The present invention  
 CC describes an immunoassay to identify agonists and antagonists, as well as  
 CC antibodies, antisense molecules and siRNAs that can all be used to bind  
 CC to and modulate expression of the cDNA molecules. As such, these  
 CC molecules are useful for diagnostic markers or therapeutic targets for  
 CC the various diseases or morbid states. In particular, they are useful in  
 CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's  
 CC disease, Parkinson's disease, dementia, short memory and various cancers,  
 CC as well as for maintaining equilibrium of sense or motor function, and  
 CC for treating emotional reaction, fear response and panic. Accordingly,  
 CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,  
 CC cyostatic and tranquiliser activities. This polypeptide is a protein  
 CC encoded by a full length human cDNA sequence of the invention. NOTE: This  
 CC sequence is not given in the sequence listing of the specification but  
 CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-  
 CC office.  
 XX  
 SQ Sequence 408 AA;  
 Query Match 100.0%; Score 358; DB 8; Length 408;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-33;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GPGDACLPAVQGPCRGWEPRWAYSPLLQQCHPFFVYGGCEGNNFHRSCEADACPVP 59  
 |||||  
 Db 214 GPGDACLPAVQGPCRGWEPRWAYSPLLQQCHPFFVYGGCEGNNFHRSCEADACPVP 272  
 |||||  
 RESULT 5  
 ABO60003  
 ID ABO60003 standard; protein; 491 AA.  
 XX  
 AC ABO60003;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human genome derived single exon protein #6237.  
 XX  
 KW Human; gene expression; single exon probe; microarray;  
 KW alternative splicing event; genomic alteration.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003194704-A1.  
 XX  
 PD 16-OCT-2003.  
 XX  
 XX 03-APR-2002; 2002US-00029386.  
 XX  
 XX 03-APR-2002; 2002US-00029386.  
 XX



XX AAG65899;  
 XX 11-FEB-2002 (first entry)  
 XX Amino acid sequence of GSK gene Id 45597.  
 XX Peptide hormone; antidiabetic; anorectic; antianorectic; antiasthmatic;  
 KW antidepressant; nootropic; neuroprotectant; hypotensive; hypertensive;  
 KW cytostatic; cerebroprotective; vasotrophic; human.  
 XX Homo sapiens.  
 XX WO200172961-A2.  
 XX 04-OCT-2001.  
 XX 22-MAR-2001; 2001WO-US009226.  
 XX 24-MAR-2000; 2000US-0192158P.  
 XX 28-MAR-2000; 2000US-0192668P.  
 XX 27-APR-2000; 2000US-0200166P.  
 XX (SMK ) SMITHKLINE BEECHAM CORP.  
 XX (SMK ) SMITHKLINE BEECHAM PLC.  
 XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;  
 PI Lai Y;  
 PI WPI; 2001-639223/73.  
 DR N-PSDB; AAI671189.  
 XX Isolated polypeptides, which may be peptide hormones, which are  
 PT identified by high throughput genome-based biology which identifies genes  
 PT and gene products as therapeutic targets for treatment of diseases such  
 PT as diabetes and cancer.  
 XX Claim 1; Page 76-77; 99pp; English.  
 XX The invention provides polypeptides (AAG65886-65918) which may be peptide  
 CC hormones (including insulin, growth hormones, chemokines, cytokines,  
 CC neuropeptides, integrins, kallikreins, lamins, melanins, natruiretic  
 CC hormones, neuropepsin, pituitary hormones, pleiotrophins, prostaglandins,  
 CC secretogranins, selectins, thromboglobulins, thymosins) identified by  
 CC high throughput genome-based biology and polynucleotides (AAI67176-67208)  
 CC encoding them. The polypeptides can be expressed by standard recombinant  
 CC methodology. The polypeptides are useful in the treatment of disease such  
 CC as diabetes, breast-, prostate-, colon cancer and other malignant tumors,  
 CC hyper- and hypotension, obesity, bulimia, anorexia, growth abnormalities,  
 CC asthma, manic depression, dementia, delirium, mental retardation,  
 CC Huntington's disease, Tourette's syndrome, schizophrenia, growth, mental  
 CC or sexual development disorders, and dysfunctions of the blood cascade  
 CC system including those leading to stroke. The polynucleotides may be used  
 CC as diagnostic reagents through detecting mutations in the associated gene  
 CC and for chromosome localization and for tissue expression studies. The  
 CC polypeptides and polynucleotides may also be used as vaccines  
 XX Sequence 548 AA;  
 SQ Query Match 100.0%; Score 358; DB 4; Length 548;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-33;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPGDACVLPAVQGPCRGWPRWASPLQQCHFPFYVGGCEGNGNNFHRSCEADACPVP 59  
 DB 354 GPGDACVLPAVQGPCRGWPRWASPLQQCHFPFYVGGCEGNGNNFHRSCEADACPVP 412  
 RESULT 8  
 ABG74120  
 ID ABG74120 standard; protein; 548 AA.  
 XX AC ABG74120;

XX 02-APR-2003 (first entry)  
 XX Human proteinase inhibitor zkun6.  
 XX Human; zkun6; proteinase inhibitor; kunitz domain; emphysema;  
 KW tissue plasminogen activator; thrombolytic therapy; CBF;  
 KW excessive proteinase activity; acute pancreatitis; deep vein thrombosis;  
 KW cardiopulmonary bypass-induced pulmonary injury; myocardial infarction;  
 KW allergy-induced proase release; shock; septic shock; psoriasis;  
 KW hyperfibrinolytic haemorrhage; rheumatoid arthritis;  
 KW adult respiratory distress syndrome; chronic inflammatory bowel disease;  
 KW inflammatory condition; platelet function; organ preservation;  
 KW wound healing; haemostasis; pulmonary embolism; post-surgical thrombosis;  
 KW blood coagulation; proteolytic tissue degradation.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 1..19 /label= Signal\_peptide  
 FT 20..548 /label= Mature\_zkun6  
 FT 33..75  
 FT /note= "Four-disulphide-core proteinase inhibitor. This  
 FT domain is specifically claimed in claim 1"  
 FT 93..157  
 FT /note= "Polistatin-type proteinase inhibitor. This  
 FT domain is specifically claimed in claim 1"  
 FT 203..286  
 FT /note= "I-set immunoglobulin domain. This domain is  
 FT specifically claimed in claim 1"  
 FT 299..351  
 FT /note= "Kunitz proteinase inhibitor domain #1. This  
 FT domain is specifically claimed in claim 1"  
 FT 359..409  
 FT /note= "Kunitz proteinase inhibitor domain #2"  
 FT 412..548  
 FT /label= Netrin domain  
 FT /note= "This domain is specifically claimed in claim 1"  
 XX US2002146789-A1.  
 XX 10-OCT-2002.  
 XX 27-MAR-2001; 2001US-00819136.  
 XX 31-MAR-2000; 2000US-0193642P.  
 XX (CONK/) CONKLIN D C.  
 XX (GAOZ/) GAO Z.  
 XX Conklin DC, Gao Z;  
 XX WPI; 2003-182404/18.  
 DR N-PSDB; ABX16035.  
 XX Isolated protein used as components of cell culture media, in protein  
 PT purification, and in certain therapeutic and diagnostic applications  
 PT comprises portion of amino acids sequence.  
 XX Claim 1; Page 17-19; 33pp; English.  
 XX The invention relates to an isolated protein (zkun6) comprising a portion  
 CC of the sequence appearing as ABG74120. The portion consists of 33-75  
 CC amino acids, 93-157 amino acids, 203-286 amino acids, 299-351 amino acids  
 CC or 412-548 amino acids. Also included are: (a) an expression vector  
 CC comprising, operably linked, a transcription promoter; a DNA segment  
 CC encoding a protein comprising one of the portions listed above (plus  
 CC amino acids 1-19); and a transcription terminator; (b) a cultured cell  
 CC containing the expression vector, where the cell expresses the DNA  
 CC segment; (c) a method of making a protein comprising culturing the cell  
 CC and (d) an antibody that specifically binds to the protein. The

CC \* proteinase inhibitor or its fragments may be used as components of cell  
 CC culture media, in protein purification, and in certain therapeutic and  
 CC diagnostic applications. The zkun6 protein may be used in combination  
 CC with tissue plasminogen activator in thrombolytic therapy. It is used in  
 CC the treatment or prevention of conditions associated with excessive  
 CC proteinase activity. Such conditions include acute pancreatitis,  
 CC cardiopulmonary bypass (CPB)-induced pulmonary injury, allergy-induced  
 CC protease release, deep vein thrombosis, myocardial infarction, shock  
 CC (including septic shock), hyperfibrinolytic haemorrhage, emphysema,  
 CC rheumatoid arthritis, adult respiratory distress syndrome, chronic  
 CC inflammatory bowel disease, psoriasis, and other inflammatory conditions.  
 CC The zkun6 protein may be used in preservation of platelet function, organ  
 CC preservation, or wound healing. It may be useful in the treatment of  
 CC conditions arising from imbalance in haemostasis. It may be used in the  
 CC treatment or prevention of pulmonary embolism, and post-surgical  
 CC thrombosis. It may be used for inhibiting blood coagulation in mammals.  
 CC It may find therapeutic use in the blockage of proteolytic tissue  
 CC degradation. The present sequence represents human zkun6 (a kunitz domain  
 CC protein)

XX Sequence 548 AA;

Query Match 100.0%; Score 358; DB 6; Length 548;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-33;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGDACVLPAVQGPCRGWEPRWAYSPILQQCHPFFVYGGCEGNGNNFHSRSCEDACPV 59  
 Db 354 GPGDACVLPAVQGPCRGWEPRWAYSPILQQCHPFFVYGGCEGNGNNFHSRSCEDACPV 412

RESULT 9

AAE39463

ID AAE39463 standard; protein; 548 AA.

AC AAE39463;

DT 18-DEC-2003 (first entry)

DE Human GDF-associated serum protein (GASP)2 protein.

XX Human; GDF-associated serum protein; GASP; amytrophic lateral sclerosis;  
 KW growth and differentiation factor; GDF; chronic glucocorticoid therapy;  
 KW familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder;  
 KW progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty;  
 KW bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome;  
 KW muscular dystrophy; congestive obstructive pulmonary disease; cachexia;  
 KW carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency;  
 KW nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopaenia;  
 KW androgen suppression; myasthenia gravis; hyperglycaemia; organ atrophy;  
 KW metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;  
 KW myotonia; neuroprotective; obesity; immunomodulator; diabetes.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 92..157

FT /note= "Follistatin domain"

FN US2003162714-A1.

XX 28-AUG-2003.

XX 21-FEB-2003; 2003US-00369736.

XX 21-FEB-2002; 2002US-0357845P.

XX 20-DEC-2002; 2002US-0434644P.

XX (AMHP ) WYETH.

XX Hill JJ, Wolfman NM;

XX WPI; 2003-756055/71.

DR N-PSDB; AAD59928.

XX Composition containing growth and differentiation factor-associated serum  
 PT protein-1, useful for treating e.g. muscular dystrophy or diabetes, also  
 PT for diagnosis.

PS Disclosure; Fig 9B; Opp; English.

XX The present invention relates to the use of a protein GDF (growth and  
 CC differentiation factor)-associated serum protein (GASP) 1 comprising  
 CC at least one follistatin domain to modulate the level or activity of  
 CC growth and differentiation factor (GDF) -8. Administration of GASP1 is  
 CC used to modulate GDF-8 for treatment of muscular disorders such as  
 CC muscular dystrophy (benign X-linked limb-girdle, facioscapulohumeral,  
 CC myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),  
 CC progressive dystrophic ophthalmoplegia, amytrophic lateral sclerosis,  
 CC congestive obstructive pulmonary disease, congenital myopathy (myotonia),  
 CC familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,  
 CC Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,  
 CC carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia  
 CC and other muscle wasting syndromes such as traumatic or chronic injury to  
 CC muscle, metabolic disorders such as diabetes types 1 or 2, impaired  
 CC glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance  
 CC induced by trauma and obesity, adipose tissue disorder such as obesity,  
 CC and bone degenerative conditions such as osteoporosis, osteopaenia,  
 CC osteoarthritis, low bone mass due to chronic glucocorticoid therapy,  
 CC premature gonadal failure, vitamin D deficiency, androgen suppression,  
 CC secondary hyperparathyroidism, nutritional deficiencies and anorexia  
 CC nervosa. The present sequence is human GDF (growth and differentiation  
 CC factor)-associated serum protein (GASP)

XX Sequence 548 AA;

Query Match 100.0%; Score 358; DB 7; Length 548;

Best Local Similarity 100.0%; Pred. No. 4.5e-33;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGDACVLPAVQGPCRGWEPRWAYSPILQQCHPFFVYGGCEGNGNNFHSRSCEDACPV 59

Db 354 GPGDACVLPAVQGPCRGWEPRWAYSPILQQCHPFFVYGGCEGNGNNFHSRSCEDACPV 412

RESULT 10

ADD93678

ID ADD93678 standard; protein; 548 AA.

XX ADD93678;

DT 29-JAN-2004 (first entry)

DE Human GDF-associated serum protein 2 (GASP2).

XX Human; GDF-associated serum protein 2; GASP2; antidiabetic; anorectic;  
 KW osteopathic; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 92..157

FT /note= Follistatin domain

FN WO2003072714-A2.

XX 04-SEP-2003.

XX 21-FEB-2003; 2003WO-US005150.

XX 21-FEB-2002; 2002US-0357846P.

XX 20-DEC-2002; 2002US-0434645P.

XX (AMHP ) WYETH.

XX Hill JJ, Wolfman NM;

```

XX WPI; 2003-812402/76.
DR N-PSDB; ADD93677.
XX
PT New compositions comprising a protein containing at least one follistatin
PT domain, useful for treating muscular dystrophy (e.g. sarcopenia, and
PT cachexia), metabolic disease (e.g. diabetes or obesity), or bone
PT degenerative diseases.
XX
PS Disclosure; Fig 9B; 113pp; English.
XX
CC The present sequence is the protein sequence for human GDF-associated
CC serum protein 2 (GASP2), a protein which includes a follistatin domain
CC and which binds to growth and differentiation factor-8 (GDF-8 or
CC myostatin). The invention provides methods for modulating the effects of
CC GDF-8 on cells. These methods involve administering a protein comprising
CC at least one follistatin domain (e.g. GASP2), or a nucleic acid encoding
CC such a protein. The methods are used to treat disorders relating to the
CC level or activity of GDF-8. These include a muscular disorder such as
CC muscular dystrophy (e.g. severe or benign X-linked muscular dystrophy,
CC limb-girdle dystrophy, facioscapulohumeral dystrophy, myotonic dystrophy,
CC distal muscular dystrophy, progressive dystrophic ophthalmoplegia,
CC oculopharyngeal dystrophy, Fukuyama-type congenital muscular dystrophy,
CC congenital myopathy, myotonia congenital, familial periodic paralysis,
CC paroxysmal myoglobinuria, myasthenia gravis, Eaton-Lambert syndrome,
CC secondary myasthenia, denervation atrophy, paroxymal muscle atrophy,
CC muscle wasting syndrome, sarcopenia, and cachexia), traumatic or chronic
CC injury to muscle tissue, metabolic disease or disorder (e.g. type 2
CC diabetes, non-insulin-dependent diabetes mellitus, hyperglycaemia, or
CC obesity), adipose tissue disorder (e.g. obesity), and bone degenerative
CC disease (e.g. osteoporosis) (all claimed).
XX
SQ Sequence 548 AA;
    Query Match      100.0%; Score 358; DB 7; Length 548;
    Best Local Similarity 100.0%; Pred. No. 4.5e-33;
    Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    OY 1 GPGDACVLPAVQGPCRGWEPRWYSPLLQQCHPFFYGGCEGNGNNFHRSCEADACPVP 59
    DB 354 GPGDACVLPAVQGPCRGWEPRWYSPLLQQCHPFFYGGCEGNGNNFHRSCEADACPVP 412

RESULT 11
AEA22339
ID AEA22339 standard; protein; 548 AA.
XX
AC AEA22339;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human GASP2 protein - SEQ ID 11.
XX
KW growth differentiation factor 8-associated serum protein 2; GASP2;
KW muscle disease; muscular-gen.; muscular dystrophy; bone disease;
KW osteopathic; osteoporosis; metabolic disorder; metabolic;
KW insulin-dependent diabetes mellitus; antidiabetic.
XX
OS Homo sapiens.
XX
PN US2005106154-A1.
XX
PD 19-MAY-2005.
XX
PF 04-JAN-2005; 2005US-00028058.
XX
PR 21-FEB-2002; 2002US-0357845P.
XX
PR 20-DEC-2002; 2002US-0434644P.
XX
PR 21-FEB-2003; 2003US-00369736.
XX
PA (AMHP ) WYETH.
XX
PI Hill JU, Wolfman NM;
XX
DR WPI; 2003-756055/71.
DR N-PSDB; AAD59927.

XX WPI; 2005-354774/36.
DR N-PSDB; AEA22338.
XX
PT New pharmaceutical compositions having a growth and differentiation
PT factor-8-associated serum protein 1, useful for treating muscular
PT dystrophy, amyotrophic lateral sclerosis, diabetes, obesity and bone
PT disorders.
XX
PS Disclosure; SEQ ID NO 11; 71pp; English.
XX
CC The invention comprises a pharmaceutical composition which contains a
CC growth differentiation factor 8 (GDF)-associated serum protein 1 (GASP1).
CC The pharmaceutical composition of the invention is useful for the
CC diagnosis, prevention and treatment of muscular disorders (e.g. muscular
CC dystrophy), bone degenerative diseases (e.g. osteoporosis), and metabolic
CC disorders (e.g. insulin-dependent diabetes mellitus). The present amino
CC acid sequence represents a human GASP2 protein.
XX
SQ Sequence 548 AA;
    Query Match      100.0%; Score 358; DB 9; Length 548;
    Best Local Similarity 100.0%; Pred. No. 4.5e-33;
    Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    OY 1 GPGDACVLPAVQGPCRGWEPRWYSPLLQQCHPFFYGGCEGNGNNFHRSCEADACPVP 59
    DB 354 GPGDACVLPAVQGPCRGWEPRWYSPLLQQCHPFFYGGCEGNGNNFHRSCEADACPVP 412

RESULT 12
AEA39462
ID AAE39462 standard; protein; 552 AA.
XX
AC AAE39462;
XX
DT 18-DEC-2003 (first entry)
XX
DE Mouse GDF-associated serum protein (GASP)2 protein.
XX
KW Mouse; GDF-associated serum protein; GASP; amyotrophic lateral sclerosis;
KW growth and differentiation factor; GDF; chronic glucocorticoid therapy;
KW familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder;
KW progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty;
KW bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome;
KW muscular dystrophy; congestive obstructive pulmonary disease; cachexia;
KW carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency;
KW nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopenia;
KW androgen suppression; myasthenia gravis; hyperglycaemia; organ atrophy;
KW metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
KW myotonia; neuroprotective; obesity; immunomodulator; diabetes.
XX
OS Mus sp.
XX
KW Key Location/Qualifiers
FT Domain 96..161
FT /note="Follistatin domain"
XX
PN US2003162714-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003US-00369736.
XX
PR 21-FEB-2002; 2002US-0357845P.
XX
PR 20-DEC-2002; 2002US-0434644P.
XX
PA (AMHP ) WYETH.
XX
PI Hill JU, Wolfman NM;
XX
DR WPI; 2003-756055/71.
DR N-PSDB; AAD59927.

```

XX Composition containing growth and differentiation factor-associated serum  
 PT protein-1, useful for treating e.g. muscular dystrophy or diabetes, also  
 PT for diagnosis.  
 XX  
 XX Disclosure; Fig 8B; Opp; English.  
 XX  
 CC The present invention relates to the use of a protein GDF (growth and  
 CC differentiation factor)-associated serum protein (GASP) 1 comprising  
 CC at least one follistatin domain to modulate the level or activity of  
 CC growth and differentiation factor (GDF) -8. Administration of GASP1 is  
 CC used to modulate GDF-8 for treatment of muscular disorders such as  
 CC muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,  
 CC myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),  
 CC progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,  
 CC congestive obstructive pulmonary disease, congenital myopathy (myotonia),  
 CC familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,  
 CC Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,  
 CC carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia  
 CC and other muscle wasting syndromes such as traumatic or chronic injury to  
 CC muscle, metabolic disorders such as diabetes types 1 or 2, impaired  
 CC glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance  
 CC induced by trauma and obesity, adipose tissue disorder such as obesity,  
 CC and bone degenerative conditions such as osteoporosis, osteopaenia,  
 CC osteoarthritis, low bone mass due to chronic glucocorticoid therapy,  
 CC premature gonadal failure, vitamin D deficiency, androgen suppression,  
 CC secondary hyperparathyroidism, nutritional deficiencies and anorexia  
 CC nervosa. The present sequence is mouse GDF (growth and differentiation  
 CC factor)-associated serum protein (GASP)  
 XX  
 XX Sequence 552 AA;

Query Match 90.2%; Score 323; DB 7; Length 552;  
 Best Local Similarity 88.1%; Pred. No. 5.6e-29;  
 Matches 52; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 GPGDACVLPAVQGPCRGWEPRWYSPLLQQCHPPFVYGCCEGNNFHSRESCDACPVP 59  
 DB 358 GPGDVICALPAVQGPCQGWEPWYSPLLQQCHPPFVYSCGEGNSNNFETRESCDACPVP 416

RESULT 13  
 ID ADD93676  
 XX  
 XX ADD93676 standard; protein; 552 AA.  
 XX  
 XX ADD93676;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Mouse GDF-associated serum protein 2 (GASP2).  
 XX  
 KW Mouse; GDF-associated serum protein 2; GASP2; antidiabetic; anorectic;  
 KW osteopathic; gene therapy.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 96..161  
 FT /note = Follistatin domain  
 XX  
 PN WO2003072714-A2.  
 XX  
 PD 04-SEP-2003.  
 XX  
 XX 21-FEB-2003; 2003WO-US005150.  
 XX  
 XX 21-FEB-2002; 2002US-0357846P.  
 PR 20-DEC-2002; 2002US-0434645P.  
 XX  
 XX (AMHP ) WYETH.  
 PA  
 XX Hill JJ, Wolfman NM;  
 XX  
 XX

DR WPI; 2003-812402/76.  
 DR N-PSDB; ADD93675.  
 XX  
 PT New compositions comprising a protein containing at least one follistatin  
 PT domain, useful for treating muscular dystrophy (e.g. sarcopenia, and  
 PT cachexia), metabolic disease (e.g. diabetes or obesity), or bone  
 PT degenerative diseases.  
 XX  
 XX Disclosure; Fig 8B; 113pp; English.  
 PS  
 XX The present sequence is the protein sequence for mouse GDF-associated  
 CC serum protein 2 (GASP2), a protein which includes a follistatin domain  
 CC and which binds to growth and differentiation factor-8 (GDF-8 or  
 CC myostatin). The invention provides methods for modulating the effects of  
 CC GDF-8 on cells. These methods involve administering a protein comprising  
 CC at least one follistatin domain (e.g. GASP2), or a nucleic acid encoding  
 CC such a protein. The methods are used to treat disorders relating to the  
 CC level or activity of GDF-8. These include a muscular disorder such as  
 CC muscular dystrophy (e.g. severe or benign X-linked muscular dystrophy,  
 CC limb-girdle dystrophy, facioscapulohumeral dystrophy, myotonic dystrophy,  
 CC distal muscular dystrophy, progressive dystrophic ophthalmoplegia,  
 CC oculopharyngeal dystrophy, Fukuyama-type congenital muscular dystrophy,  
 CC congenital myopathy, myotonia congenital, familial periodic paralysis,  
 CC paroxysmal myoglobinuria, myasthenia gravis, Eaton-Lambert syndrome,  
 CC secondary myasthenia, denervation atrophy, paroxysmal muscle atrophy,  
 CC muscle wasting syndrome, sarcopenia, and cachexia), traumatic or chronic  
 CC injury to muscle tissue, metabolic disease or disorder (e.g. type 2  
 CC diabetes, non-insulin-dependent diabetes mellitus, hyperglycaemia, or  
 CC obesity), adipose tissue disorder (e.g. obesity), and bone degenerative  
 CC disease (e.g. osteoporosis) (all claimed).  
 XX  
 XX Sequence 552 AA;

Query Match 90.2%; Score 323; DB 7; Length 552;  
 Best Local Similarity 88.1%; Pred. No. 5.6e-29;  
 Matches 52; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 GPGDACVLPAVQGPCRGWEPRWYSPLLQQCHPPFVYGCCEGNNFHSRESCDACPVP 59  
 DB 358 GPGDVICALPAVQGPCQGWEPWYSPLLQQCHPPFVYSCGEGNSNNFETRESCDACPVP 416

RESULT 14  
 AEA22337  
 ID AEA22337 standard; protein; 552 AA.  
 XX  
 XX AEA22337;  
 XX  
 DT 28-JUL-2005 (first entry)  
 XX  
 DE Mouse GASP2 protein - SEQ ID 9.  
 XX  
 KW growth differentiation factor 8-associated serum protein 2; GASP2;  
 KW muscle disease; muscular-gen.; muscular dystrophy; bone disease;  
 KW osteopathic; osteoporosis; metabolic disorder; metabolic;  
 KW insulin-dependent diabetes mellitus; antidiabetic.  
 XX  
 OS Mus sp.  
 OS  
 PN US2005106154-A1.  
 XX  
 PD 19-MAY-2005.  
 XX  
 XX 04-JAN-2005; 2005US-00028058.  
 PF  
 XX 21-FEB-2002; 2002US-0357845P.  
 PR 20-DEC-2002; 2002US-0434644P.  
 PR 21-FEB-2003; 2003US-00369736.  
 XX  
 XX (AMHP ) WYETH.  
 PA  
 XX Hill JJ, Wolfman NM;  
 XX  
 XX



DR WPI; 2005-354774/36.  
XX N-PSDB; ABA22336.  
XX  
PT New pharmaceutical compositions having a growth and differentiation  
factor-8-associated serum protein 1, useful for treating muscular  
PT dystrophy, amyotrophic lateral sclerosis, diabetes, obesity and bone  
PT disorders.  
XX  
XX  
PS Disclosure; SEQ ID NO 9; 71pp; English.  
XX  
CC The invention comprises a pharmaceutical composition which contains a  
growth differentiation factor 8 (GDF)-associated serum protein 1 (GASp1).  
CC The pharmaceutical composition of the invention is useful for the  
diagnosis, prevention and treatment of muscular disorders (e.g. muscular  
dystrophy), bone degenerative diseases (e.g. osteoporosis), and metabolic  
disorders (e.g. insulin-dependent diabetes mellitus). The present amino  
acid sequence represents a mouse GASp2 protein.  
XX  
SQ Sequence 552 AA;  
Query Match 90.2%; Score 323; DB 9; Length 552;  
Best Local Similarity 88.1%; Pred. No. 5.6e-29;  
Matches 52; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GPGDACVLPAVQGPCRGWEPRWAYSPLQQCHPFPVYGGCEGNGNNFHRSCEDEDACPV 59  
DB 358 GPGDVCLPAVQGPCQGWEPWAYSPLLQQCHPFPVYSGCEGNSNNFETRESCEDEDACPV 416  
RESULT 15  
ADG36986  
ID ADG36986 standard; protein; 283 AA.  
XX  
XX AC ADG36986;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Kunitz type serine protease inhibitory protein related protein.  
XX  
XX antiinflammatory; Gene therapy; Ki316;  
KW serine protease inhibitory protein; inflammatory disease; human;  
KW kunitz type serine protease inhibitor.  
XX  
XX Unidentified.  
XX OS  
XX JP2003235574-A.  
XX PN  
XX 26-AUG-2003.  
XX PD  
XX 15-FEB-2002; 2002JP-00038074.  
XX PF  
XX 15-FEB-2002; 2002JP-00038074.  
XX PR  
XX (MOCH ) MOCHIDA PHARM CO LTD.  
XX PA  
XX WPI; 2004-002192/01.  
XX DR  
XX N-PSDB; ADG36985.  
XX  
PT Novel DNA Ki316 which codes serine protease inhibitory protein Ki316,  
PT useful for diagnosing and treating Ki316 related diseases e.g.  
PT inflammatory diseases.  
XX  
XX Example 1; SEQ ID NO 4; 25pp; Japanese.  
XX  
CC The invention describes a Ki316 DNA (I) having a fully defined sequence  
(SI) of 2154 bp as given in the specification or a DNA which hybridises  
to (SI) under stringent conditions and encoding a serine protease  
inhibitory protein. (I) is useful for treating inflammatory diseases. (I)  
efficiently prevents onset of inflammatory diseases. This is the amino  
acid sequence of a novel human kunitz type serine protease inhibitory  
protein Ki316 related protein.  
XX  
SQ Sequence 283 AA;

Query Match 66.8%; Score 239; DB 8; Length 283;  
Best Local Similarity 66.1%; Pred. No. 1.8e-19;  
Matches 39; Conservative 7; Mismatches 13; Indels 0; Gaps 0;  
QY 1 GPGDACVLPAVQGPCRGWEPRWAYSPLQQCHPFPVYGGCEGNGNNFHRSCEDEDACPV 59  
DB 88 GPLAACSLPALQGPCKAYAPRWAYNSQTGCQCSFVYGGCEGNGNNFESREACESCPFP 146  
Search completed: February 16, 2006, 18:29:24  
Job time : 190 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 16, 2006, 18:29:41 ; Search time 38 Seconds  
(without alignments)  
149.389 Million cell updates/sec

Title: US-10-021-963-2

Perfect score: 358

Sequence: 1 GPGDACVLPAVQGPCRGWEP.....EGNGNNFHSRSCDACPVP 59

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	174	48.6	349	2	alpha-1-microglobu
2	171	47.8	337	1	alpha-1-microglobu
3	170	47.5	352	1	alpha-1-microglobu
4	169	47.2	110	1	basic proteinase i
5	167.5	46.8	62	2	proteinase inhibit
6	166	46.4	349	2	alpha-1-microglobu
7	165	46.1	123	2	inter-alpha-trypsi
8	165	46.1	125	1	alpha-1-microglobu
9	164	45.8	252	2	hepatocyte growth
10	163	45.5	235	2	tissue factor path
11	163	45.5	352	1	alpha-1-microglobu
12	158	44.1	61	1	proteinase inhibit
13	157.5	44.0	2944	2	collagen alpha 1(V
14	155	43.3	2225	2	hypothetical prote
15	154	43.0	1549	2	type VII collagen
16	152	42.5	1558	2	protein C37C3.6a [
17	152	42.5	2167	2	hypothetical prote
18	150	41.9	67	1	trypsin inhibitor,
19	149	41.6	63	1	acrosin inhibitor
20	145	40.5	57	2	basic proteinase i
21	145	40.5	62	2	taicatoxin erine
22	145	40.5	65	1	venom basic protei
23	144	40.2	299	2	tissue factor path
24	144	40.2	300	2	lipoprotein-associ
25	144	40.2	396	2	tissue factor path
26	140	39.1	62	2	venom basic protei
27	138.5	38.7	3176	2	collagen alpha 3(V
28	138	38.5	304	1	tissue factor path
29	137	38.3	302	1	tissue factor path

## ALIGNMENTS

### RESULT 1

S21089

alpha-1-microglobulin/inter-alpha-trypsin inhibitor light chain precursor - rat  
N/Alternate names: acid-stable proteinase inhibitor; bikunin; trypstatin  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 22-Nov-1993 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004

C/Accession: S21089; A53056; A25935; A31890; A61633

R/Lindqvist, A.; Bratt, T.; Altieri, M.; Kastern, W.; Akerstroem, B.

Biochim. Biophys. Acta 1130, 63-67, 1992

A/Title: Rat alpha(1)-microglobulin: co-expression in liver with the light chain of inte

A/Reference number: S21089; MUID:92182014; PMID:1371936

A/Accession: S21089

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-349 <LIN>

A/Cross-references: UNIPROT:Q64240; UNIPARC:UPI000004B357; GB:S87544; NID:G247162; PIDN

R/Itoh, H.; Ide, H.; Ishikawa, N.; Nawa, Y.

J. Biol. Chem. 269, 3818-3822, 1994

A/Title: Mast cell protease inhibitor, trypstatin, is a fragment of inter-alpha-trypsin

A/Reference number: A53056; MUID:94148892; PMID:7508921

A/Accession: A53056

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 285-341 <ITO>

A/Cross-references: UNIPARC:UPI00001762B6

R/Kastern, W.; Bjorck, L.; Akerstroem, B.

J. Biol. Chem. 261, 15070-15074, 1986

A/Title: Developmental and tissue-specific expression of alpha-1-microglobulin mRNA in t

A/Reference number: A25935; MUID:87033744; PMID:2429963

A/Accession: A25935

A/Molecule type: protein

A/Residues: 141,'A',143-195 <KAS>

A/Cross-references: UNIPARC:UPI0000170A10

R/Kido, H.; Yokogoshi, Y.; Katunuma, N.

J. Biol. Chem. 263, 18104-18107, 1988

A/Title: Kunitz-type protease inhibitor found in rat mast cells. Purification, properties

A/Reference number: A31890; MUID:89053978; PMID:3263966

A/Accession: A31890

A/Molecule type: protein

A/Residues: 283-301,'L',303-322,'N',324-329,'PK',332-333,'W',335-343 <KID>

A/Cross-references: UNIPARC:UPI000014676D

R/Sugiki, M.; Maruyama, M.; Yoshida, E.; Sumi, H.; Mihara, H.

Inflammation 15, 281-289, 1991

A/Title: Acid-stable protease inhibitor in chronic phase of carrageenin-induced inflamma

A/Reference number: A61633; MUID:92120777; PMID:1769732

A/Accession: A61633

A/Molecule type: protein

A/Residues: 205-213,'X',215-229,'N',231-232,'K',234-238 <SUG>

A/Cross-references: UNIPARC:UPI00001762B7

C/Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu

C/Keywords: chondroitin sulfate proteoglycan; chromoprotein; glycoprotein; plasma; serin

F/I-19/Domain: signal sequence #status predicted <SIG>



C;Accession: A01224  
 R;Kato, I.; Tominaga, N.  
 Fed. Proc. 38, 832, 1979  
 A;Title: Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tandem repeats of a 110 amino acid residue unit  
 A;Reference number: A01224  
 A;Accession: A01224  
 A;Molecule type: protein  
 A;Residues: 1-110 <KAT>  
 A;Cross-references: UNIPROT:P00993; UNIPARC:UPI000012D12B  
 C;Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain  
 C;Superfamily: logerhead basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor  
 C;Keywords: pyroglutamic acid; serine proteinase inhibitor  
 F;18-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>  
 F;63-105/Domain: antileukoproteinase repeat homology <ALP>  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8-58,17-41,33-54,67-93,76-97,80-92,86-101/disulfide bonds: #status predicted  
 F;18/Inhibitory site: Lys (trypsin) #status predicted

Query Match 47.2%; Score 169; DB 1; Length 110;  
 Best Local Similarity 50.0%; Pred. No. 5.6e-12;  
 Matches 28; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 4 DACVLPAVQGPCRGWEPWYSPLLQQCHPFFVYGCNGNHFHRESCEDACPVP 59  
 Db 6 DICRLPPQGPCKGRIPRYFNPASRMCESEFYGGCKGNKNFKTKAEVCVRACRP 61

RESULT 5  
 S07451  
 proteinase inhibitor 5.II - snake-locks sea anemone  
 C;Species: Anemonia sulcata (snake-locks sea anemone)  
 C;Date: 31-Dec-1990 #sequence\_revision 09-May-1997 #text\_change 09-Jul-2004  
 C;Accession: S07451; B27222  
 R;Wunderer, G.; Machleidt, W.; Fritz, H.  
 Meth. Enzymol. 80, 815-820, 1981  
 A;Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia  
 A;Reference number: S07451  
 A;Accession: S07451  
 A;Molecule type: protein  
 A;Residues: 1-59 <WUN>  
 A;Cross-references: UNIPROT:P10280; UNIPARC:UPI00001762AE  
 A;Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found  
 R;Krebs, H.C.; Habermehl, G.G.  
 Naturwissenschaften 74, 395-396, 1987  
 A;Title: Isolierung und strukturaufklaerung eines haemolytisch aktiven peptids aus der  
 A;Reference number: A94700  
 A;Accession: B27222  
 A;Molecule type: protein  
 A;Residues: 1-38, 'R', '40', 'B', '42', 'BB', '45-48', 'ZZ', '51', 'Z', '53-62 <KRE>  
 A;Cross-references: UNIPARC:UPI00001762AF  
 C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol  
 C;Keywords: serine proteinase inhibitor  
 F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.8%; Score 167.5; DB 2; Length 62;  
 Best Local Similarity 53.6%; Pred. No. 4.8e-12;  
 Matches 30; Conservative 6; Mismatches 19; Indels 1; Gaps 1;

Qy 3 GDACVLPAVQGPCRGWEPWYSPLLQQCHPFFVYGCNGNHFHRESCEDACPVP 58  
 Db 3 GD-CBLPKVVGPCRRPFRYYNSSSKRCEKFIYGGCGGNANFHTLECEKVGCV 57

RESULT 6  
 S35708  
 alpha-1-microglobulin / bikunin precursor - mouse  
 N;Alternate names: alpha 1-microglobulin / inter-alpha-trypsin inhibitor light chain  
 C;Species: Mus musculus (house mouse)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C;Accession: S35708; JX0355  
 R;Chan, P.; Salier, J.F.  
 Biochim. Biophys. Acta 1174, 195-200, 1993  
 A;Title: Mouse alpha-1-microglobulin/bikunin precursor: cDNA analysis, gene evolution and

A;Reference number: S35708; MUID:93363639; PMID:7689339  
 A;Accession: S35708  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-349 <CHA>  
 A;Cross-references: UNIPROT:Q07456; UNIPARC:UPI0000027CS2; EMBL:X68680; NID:9311702; PID  
 R;Itch, H.; Ide, H.; Kataoka, H.; Tomita, M.; Yoshihara, H.; Nawa, Y.  
 J. Biochem. 116, 767-772, 1994  
 A;Title: cDNA sequencing of mouse alpha1-microglobulin/inter-alpha-trypsin inhibitor lig  
 A;Reference number: JX0355; MUID:95189774; PMID:7533761  
 A;Accession: JX0355  
 A;Molecule type: mRNA  
 A;Residues: 1-64, 'S', '66-349 <ITO>  
 A;Cross-references: UNIPARC:UPI0000022E75; DBJ:D28812; NID:9556530; PIDN:BAA05973.1; PI  
 A;Experimental source: liver  
 C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu  
 C;Keywords: glycoprotein; inflammation; serine proteinase inhibitor  
 F;34-187/Domain: lipocalin homology <LIP>  
 F;230-280/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>  
 F;286-336/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
 F;114,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.4%; Score 166; DB 2; Length 349;  
 Best Local Similarity 50.9%; Pred. No. 3.6e-11;  
 Matches 28; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 5 ACVLPAVQGPCRGWEPWYSPLLQQCHPFFVYGCNGNHFHRESCEDACPVP 59  
 Db 285 ACNLPVQGPCRGAFIKLWAFDAQKQCIQPHYGCKGNKGFYSEKCEKCYGVP 339

RESULT 7  
 A29652  
 inter-alpha-trypsin inhibitor (BPI type) - sheep (fragment)  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
 C;Accession: A29652  
 R;Raap, G.; Hochstrasser, K.; Wachter, E.; Reisinger, P.W.M.  
 Biol. Chem. Hoppe-Seyler 368, 727-731, 1987  
 A;Title: The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha  
 sin inhibitor, XI.)  
 A;Reference number: A29652; MUID:87299012; PMID:2441725  
 A;Accession: A29652  
 A;Molecule type: protein  
 A;Residues: 1-123 <RAS>  
 A;Cross-references: UNIPROT:P13371; UNIPARC:UPI000012D0D9  
 C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu  
 C;Keywords: serine proteinase inhibitor  
 F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>  
 F;61-111/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Query Match 46.1%; Score 165; DB 2; Length 123;  
 Best Local Similarity 47.3%; Pred. No. 1.7e-11;  
 Matches 26; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 5 ACVLPAVQGPCRGWEPWYSPLLQQCHPFFVYGCNGNHFHRESCEDACPVP 59  
 Db 60 ACNLPVQGPCRGELWAFDAVKGKCVRFYGGCGNGNGFYSQKECKCYGIP 114

RESULT 8  
 TIH0BI  
 alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)  
 N;Alternate names: E1-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI  
 C;Species: Equus caballus (domestic horse)  
 C;Date: 30-Jun-1987 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
 C;Accession: A01210; A45653  
 R;Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.  
 Biol. Chem. Hoppe-Seyler 366, 473-478, 1985  
 A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a  
 A;Reference number: A90685; MUID:85225967; PMID:2408637  
 A;Accession: A01210  
 A;Molecule type: protein



A;Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene  
A;Reference number: S10778; MUID:90336621; PMID:1696200  
A;Accession: S10778  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-202 <DIA>  
A;Cross-references: UNIPARC:UPI000017315C  
R;Kameyer, J.F.; Polazzi, J.O.; Kotick, M.P.  
Nucleic Acids Res. 14, 7839-7850, 1986  
A;Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-  
A;Reference number: A93642; MUID:87040757; PMID:2430261  
A;Accession: A93642  
A;Molecule type: mRNA  
A;Residues: 1-352 <KAU>  
A;Cross-references: UNIPARC:UPI0000009AF; GB:X04494; NID:924478; PIDN:CAA28182.1; PID:9  
R;Lopez Otin, C.; Grubb, A.O.; Mendez, E.  
Arch. Biochem. Biophys. 228, 544-554, 1984  
A;Title: The complete amino acid sequence of human complex-forming glycoprotein heteroge  
A;Reference number: A90074; MUID:84126849; PMID:6198962  
A;Accession: A90074  
A;Molecule type: protein  
A;Residues: 20-56;58-202 <LOP>  
A;Cross-references: UNIPARC:UPI000017315D  
A;Experimental source: individual with tubular proteinuria  
A;Note: no evidence of sequence heterogeneity could be found, in spite of persistent he  
R;Takagi, T.; Takagi, K.; Kawai, T.  
Biochem. Biophys. Res. Commun. 98, 997-1001, 1981  
A;Title: Complete amino acid sequence of human alpha-1-microglobulin.  
A;Reference number: A90225; MUID:81184038; PMID:6164372  
A;Accession: A90225  
A;Molecule type: protein  
A;Residues: 20-47;58-136,138-141,'T',143-144,146-198 <TAK>  
A;Cross-references: UNIPARC:UPI000017315E; UNIPARC:UPI000017315F  
A;Experimental source: pooled urine of patients with tubular proteinuria  
R;Reisinger, P.; Hochrasser, K.; Albrecht, G.J.; Lempert, K.; Salter, J.P.  
Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993  
A;Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of ca  
A;Reference number: PNO450; MUID:93221481; PMID:8466493  
A;Accession: PNO450  
A;Molecule type: protein  
A;Residues: 206-290,'VI',293-342,'E',344-350 <REI>  
A;Cross-references: UNIPARC:UPI0000173160  
R;Atmanli, F.; Lacour, B.; Strecker, G.; Parvy, P.; Drueke, T.; Daudon, M.  
Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993  
A;Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of ca  
A;Reference number: PNO450; MUID:93221481; PMID:8466493  
A;Accession: PNO450  
A;Molecule type: protein  
A;Residues: 206-214,'X',216-230,'X',232-239,'X',241-248,'XX',251-252,'X',254 <MCK>  
A;Cross-references: UNIPARC:UPI0000173161  
R;Englild, J.J.; Salvessen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.  
J. Biol. Chem. 266, 747-751, 1991  
A;Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot  
A;Reference number: A93079; MUID:91093267; PMID:1898736  
A;Accession: B39079  
A;Molecule type: protein  
A;Residues: 206-225 <ENGL>  
A;Cross-references: UNIPARC:UPI0000173162  
R;Chirat, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.  
Int. J. Biochem. 23, 1201-1203, 1991  
A;Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inh  
A;Reference number: A61580; MUID:92175157; PMID:1794445  
A;Accession: A61580  
A;Molecule type: protein  
A;Residues: 214,'X',216-222,'X' <CHI>  
A;Cross-references: UNIPARC:UPI0000173163  
R;McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A.  
J. Biol. Chem. 261, 5378-5383, 1986  
A;Title: Two apparent human endothelial cell growth factors from human hepatoma cells an  
A;Reference number: A92593; MUID:86168278; PMID:3007499  
A;Accession: B25604  
A;Molecule type: protein  
A;Residues: 206-214,'X',216-230,'X',232-239,'X',241-248,'XX',251-252,'X',254 <MCK>

A;Cross-references: UNIPARC:UPI0000173164  
R;Englild, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvessen, G.  
J. Biol. Chem. 264, 15975-15981, 1989  
A;Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al  
A;Reference number: A92736; MUID:85380192; PMID:2476436  
A;Accession: C34245  
A;Molecule type: protein  
A;Residues: 206-225 <ENG2>  
A;Cross-references: UNIPARC:UPI0000173162  
R;Traboni, C.; Cortese, R.  
Nucleic Acids Res. 14, 6340, 1986  
A;Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobul  
A;Reference number: A25303; MUID:86312901; PMID:2428011  
A;Accession: A25303  
A;Molecule type: mRNA  
A;Residues: 1-218,'HW' <TRA>  
A;Cross-references: UNIPARC:UPI0000173165  
A;Note: this mRNA sequence appears to contain errors after residue 218  
R;Calero, M.; Escribano, J.; Grubb, A.; Mendez, E.  
J. Biol. Chem. 269, 384-389, 1994  
A;Title: Location of a novel type of interpolypeptide chain linkage in the human protein  
A;Reference number: A53110; MUID:94103241; PMID:7506257  
A;Accession: A53110  
A;Molecule type: protein  
A;Residues: 45-57 <CALI>  
A;Cross-references: UNIPARC:UPI0000173166  
R;Vetr, H.; Koegler, M.; Gebhard, W.  
FEBS Lett. 245, 137-140, 1989  
A;Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inh  
A;Reference number: S03552; MUID:89171290; PMID:2466696  
A;Accession: S03552  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 206-352 <VET2>  
A;Cross-references: UNIPARC:UPI0000110902  
R;Malki, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fourn  
Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992  
A;Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolation  
A;Reference number: S28928; MUID:93039735; PMID:1384548  
A;Accession: S28930  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 206-215 <NAL>  
A;Cross-references: UNIPARC:UPI000014AD5F  
R;Morille, W.; Capon, C.; Balduyck, M.; Sautiere, P.; Kouach, M.; Michalski, C.; Fourn  
Eur. J. Biochem. 221, 881-888, 1994  
A;Title: Chondroitin sulphate covalently cross-links the three polypeptide chains of int  
A;Reference number: S43466; MUID:94229087; PMID:7513643  
A;Accession: S43466  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 206-221 <MOR>  
A;Cross-references: UNIPARC:UPI0000173167  
R;Winiewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.  
Biochemistry 33, 7423-7429, 1994  
A;Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable compl  
A;Reference number: A53642; MUID:94271799; PMID:7516184  
A;Accession: A53642  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 206-217 <WIS>  
A;Cross-references: UNIPARC:UPI0000173168  
R;Calero, M.; Mendez, E.; Garcia, E.  
Biochim. Biophys. Acta 1249, 91-99, 1995  
A;Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin)  
A;Reference number: S55688; MUID:95284116; PMID:7539295  
A;Accession: S55688  
A;Molecule type: protein  
A;Residues: 20-24 <CAL2>  
A;Cross-references: UNIPARC:UPI0000173169  
R;Bourguignon, J.; Diarra-Mehrpour, M.; Sesboue, R.; Frain, M.; Sala-Trepat, J.M.; Marti  
Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985  
A;Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide se





ed and subsequently O-glycosylated.

C:Genetics: A:Gene: GDB:COL7A1; EBR1; EBD1; EB  
A:Cross-references: GDB:128750; OMIM:120120  
A:Map position: 3p21.3-3p21.3  
A:Note: defects in this gene can result in dominant and recessive dystrophic epidermolysis  
A:Note: there are 118 introns  
C:Complex: type VII collagen is probably a homotrimer  
C:Function:  
A:Description: structural component of extracellular polymer associated with anchoring fibrils  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>  
F:17-1253/Domain: amino-terminal nonhelical #status predicted <NC1>  
F:36-201/Domain: von Willebrand factor type A repeat homology <VWA1>  
F:231-318/Domain: fibronectin type III repeat homology <FN1>  
F:327-413/Domain: fibronectin type III repeat homology <FN2>  
F:414-502/Domain: fibronectin type III repeat homology <FN3>  
F:508-593/Domain: fibronectin type III repeat homology <FN4>  
F:598-683/Domain: fibronectin type III repeat homology <FN5>  
F:685-771/Domain: fibronectin type III repeat homology <FN6>  
F:776-862/Domain: fibronectin type III repeat homology <FN7>  
F:864-952/Domain: fibronectin type III repeat homology <FN8>  
F:954-1045/Domain: fibronectin type III repeat homology <FN9>  
F:1052-1219/Domain: von Willebrand factor type A repeat homology <VWA2>  
F:1170-1172/Region: cell attachment (R-G-D) motif  
F:1189-1253/Region: cysteine/proline-rich  
F:1254-2783/Region: interrupted helical  
F:1334-1336/Region: cell attachment (R-G-D) motif  
F:2008-2010/Region: cell attachment (R-G-D) motif  
F:2553-2555/Region: cell attachment (R-G-D) motif  
F:2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>  
F:2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>  
F:337,786,1109/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:2167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro) #status experimental  
F:2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental  
F:2625,2631/Binding site: carboxylate (Lys) (covalent) #status experimental  
F:2634,2802,2804/Disulfide bonds: interchain #status predicted

Query Match 44.0%; Score 157.5; DB 2; Length 2944;  
Best Local Similarity 49.1%; Pred. No. 2,4e-09;  
Matches 28; Conservative 6; Mismatches 20; Indels 3; Gaps 1;

Qy 4 DACVLPVQGPCRGWEPRW---AYSPLLQOCHPFVYGGCGGNNGNNFHSRSCEDACP 57

Db 2874 DPCSLPLDEGSGTAYTLRWYHRAVGTGSTEACHPFVYGGCGGNANRFGTRECERRCP 2930

RESULT 14

T26063  
hypothetical protein W01F3.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T26063  
R:Cummings, P.  
submitted to the EMBL Data Library, March 1997  
A:Reference number: Z20145  
A:Accession: T26063  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2225 <WIL>  
A:Cross-references: UNIPROT:O45881; UNIPARC:UPI00000816EC; EMBL:Z92815; PIDN:CAB07294.1;  
A:Experimental source: clone W01F3  
C:Genetics:  
A:Gene: CESP:W01F3.3  
A:Map position: 5  
A:Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1;

Query Match 43.3%; Score 155; DB 2; Length 2225;  
Best Local Similarity 50.0%; Pred. No. 3.5e-09;  
Matches 27; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 6 CVLPVQGPCRGWEPRWAYSPLLQOCHPFVYGGCGGNNGNNFHSRSCEDACPVP 59

Db 463 CVGSLFPGCHGSPQRYFYNEDSOKCEQFYSGCGGNNGNNYSEACEDRCAPP 516

RESULT 15

T48103  
type VII collagen - Chinese hamster (fragment)  
C:Species: Cricetulus griseus (Chinese hamster)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I48103  
R:Greenspan, D.S.  
Hum. Mol. Genet. 2, 273-278, 1993  
A:Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous  
A:Reference number: I48103; MUID:93271985; PMID:8499916  
A:Accession: I48103  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1549 <RES>  
A:Cross-references: UNIPROT:Q60444; UNIPARC:UPI00000E753D; GB:L06863; NID:G388624; PIDN:  
F:1484-1536/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 43.0%; Score 154; DB 2; Length 1549;  
Best Local Similarity 50.0%; Pred. No. 3.2e-09;  
Matches 28; Conservative 5; Mismatches 21; Indels 2; Gaps 1;

Qy 4 DACVLPVQGPCRGWEPRWAYS--PLLQOCHPFVYGGCGGNNGNNFHSRSCEDACP 57

Db 1482 DPCSLPLDEGSGTAYTLRWYHRAVPGGTACHPFVYGGCGGNANRFGTRECERRCP 1537

Search completed: February 16, 2006, 18:34:05  
Job time : 38 secs

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OM protein - protein search, using sw model

Run on: February 16, 2006, 18:26:21 ; Search time 232 Seconds  
(without alignments)  
179.423 Million cell updates/sec

Title: US-10-021-963-2

Perfect score: 358

Sequence: 1 GPGDACLPAVQGPCRGWEP.....EGNGNNFHSRESCDACPVP 59

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05\_80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	358	100.0	491	Q7LDW0	HUMAN
2	358	100.0	548	Q96NZ8	HUMAN
3	323	90.2	222	Q8R0S6	MOUSE
4	239	66.8	283	Q5ZNI4	HUMAN
5	239	66.8	576	Q8TEU8	HUMAN
6	239	66.8	576	Q6UXZ9	HUMAN
7	229	64.0	569	Q4T583	TETNG
8	227	63.4	571	Q7TQK3	MOUSE
9	226	63.1	571	Q5SUS5	MOUSE
10	216	60.3	572	Q4S5G7	TETNG
11	214	59.8	382	Q52KV4	XENLA
12	212	59.2	581	Q4S7P4	TETNG
13	188	52.5	558	Q6NUX0	BRARE
14	184	51.4	501	Q6NUV7	BRARE
15	174	48.6	349	1	AMBP RAT
16	171	47.8	337	1	AMBP PIG
17	170	47.5	346	1	AMBP MERUN
18	170	47.5	349	1	AMBP MESAU
19	170	47.5	352	1	AMBP BOVIN
20	169	47.2	110	1	IBP CARCR
21	168	46.9	759	2	Q8IT91 ANCCA
22	167.5	46.8	62	1	IP52 ANESU
23	167	46.6	2419	2	Q7PXZ1 ANOGA
24	166	46.4	349	1	AMBP MOUSE
25	166	46.4	349	2	Q925W1 MOUSE
26	166	46.4	349	2	Q9DBJ9 MOUSE
27	165	46.1	68	2	Q5REJ7 PONPY
28	165	46.1	123	1	IATR CAPHI
29	165	46.1	123	1	IATR SHEEP
30	165	46.1	125	1	IATR HORSE
31	165	46.1	352	2	Q5NVR3 PONPY

32	164	45.8	252	1	SPIT2	MOUSE
33	164	45.8	3198	2	Q9U8G8	MANDUCA SEX
34	163	45.5	151	2	P78491	HUMAN
35	163	45.5	235	1	TPPI2	HUMAN
36	163	45.5	235	2	Q66ME8	HOMO SAPIEN
37	163	45.5	352	1	AMBP	HUMAN
38	163	45.5	352	2	Q5TBD7	HUMAN
39	162	45.3	83	2	Q6ITB5	XYURANUS M
40	162	45.3	90	2	Q6T6T5	BITGA
41	162	45.3	352	2	Q70160	CAVIA PORCE
42	161.5	45.1	234	2	Q7YRQ8	BOVIN
43	161	45.0	83	2	Q6ITB4	XYURANUS M
44	161	45.0	83	2	Q6ITB6	XYURANUS S
45	160	44.7	83	2	Q90WAI	PSEUDONAJA

ALIGNMENTS

RESULT 1  
Q7LDW0 HUMAN PRELIMINARY; PRT; 491 AA.  
AC Q7LDW0;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein RJD2 (Fragment).  
GN Name=RJD2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21095910; PubMed=11157797; DOI=10.1093/hmg/10.4.339;  
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,  
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,  
RA Higgs D.R.;  
RT "Sequence, structure and pathology of the fully annotated terminal 2  
Mb of the short arm of human chromosome 16.";  
RL Hum. Mol. Genet. 10:339-352(2001).  
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.  
DR EMBL; AE006464; AAK61237.1; -; Genomic\_DNA.  
DR HSSP; Q16019; 1AAP.  
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR001134; Netrin C.  
DR InterPro; IPR011497; Prot\_inh\_Kazal\_2.  
DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
DR Pfam; PF07648; Kazal\_2\_1.  
DR Pfam; PF00014; Kunitz\_BPTI; 2.  
DR PRINTS; PR00759; BASICPTASE.  
DR PRODOM; PD000222; Prot\_inh\_Kunz-m; 2.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00408; IGc2; 1.  
DR SMART; SM00131; KU; 2.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
DR PROSITE; PS02279; BPTI\_KUNITZ\_2; 2.  
DR PROSITE; PS00835; IG LIKE; 1.  
DR PROSITE; PS0189; NTR; 1.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 491 AA; 52710 MW; 050954C8DFB66206 CRC64;

Query Match 100.0%; Score 358; DB 2; Length 491;  
Best Local Similarity 100.0%; Pred. No. 2.1e-32;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGDACLPAVQGPCRGWEPWAYSPLLQOCHPFVYGGCEGNGNNFHSRESCDACPVP 59  
|||||



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OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Tongue;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.,
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; AK131196; BAD18391.1; -; mRNA.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00131; KU; 1.
DR SMART; SM00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 283 AA; 31291 MW; 86206E7309866D30 CRC64;

Query Match 66.8%; Score 239; DB 2; Length 283;
Best Local Similarity 66.1%; Pred. No. 4.6e-19;
Matches 39; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

OY 1 GPGDACLVPAGVQPCRGWEPRWYSPLLQQCHPFFVYGGCEGNGNFFHSRSCDACPVP 59
DB 88 GPLAACSLLPALQGPCKAVAPRWYNSQTQCQSFVYGGCEGNGNFFSREACSCPP 146

RESULT 5
OY Q8TEU8 HUMAN PRELIMINARY; PRT; 576 AA.
AC Q8TEU8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multivalent protease inhibitor protein.
GN Name=WFIKN2; Synonyms=WFIKNRP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Trexler M., Banyai L., Pathy L.;
RA Trexler M., Banyai L., Pathy L.;
RT "A human protein containing multiple types of protease-inhibitory
modules."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3705-3709(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Trexler M., Banyai L., Pathy L.;
RA Trexler M., Banyai L., Pathy L.;
RT "Distinct expression pattern of two related human proteins containing
multiple types of protease-inhibitory modules."
RL Biol. Chem. 383:0-0(2002).
RA EMBL; AF468657; AAL77058.1; -; mRNA.
DR HSSP; P00974; 1K09.
DR *Ensembl; ENSG00000173714; Homo sapiens.
DR HGNC; HGNC:30916; WFIKN2.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
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DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
KW Protease.
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDBE121F81 CRC64;

Query Match 66.8%; Score 239; DB 2; Length 576;
Best Local Similarity 66.1%; Pred. No. 9.3e-19;
Matches 39; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

OY 1 GPGDACLVPAGVQPCRGWEPRWYSPLLQQCHPFFVYGGCEGNGNFFHSRSCDACPVP 59
DB 381 GPLAACSLLPALQGPCKAVAPRWYNSQTQCQSFVYGGCEGNGNFFSREACSCPP 439

RESULT 6
OY Q6UXZ9 HUMAN PRELIMINARY; PRT; 576 AA.
AC Q6UXZ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bikunin hlg.
GN Name=WFIKN2; ORFNames=UNQ9235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358142; AAQ88509.1; -; mRNA.
DR HSSP; P00974; 1K09.
DR HGNC; HGNC:30916; WFIKN2.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008197; WAP.
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DR - Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Query Match 66.8%; Score 239; DB 2; Length 576;
Best Local Similarity 66.1%; Pred. No. 9.3e-19;
Matches 39; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 GPGDACLPLAVQPCRGWEPWAYSPLLQCHPFFVYGGCGNGNNFHRSCEDEDACPVP 59
DB 381 GPLAACSLPALQGPCKAYAPWAYNSQTQCQSFVYGGCGNGNNFHRSCEBSCPPF 439

RESULT 7
Q4T583_TETNG
ID Q4T583_TETNG PRELIMINARY; PRT; 569 AA.
AC Q4T583;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF9360, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0006943001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Maudel E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattoilco L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; CAEE01009360; CAF91949.1; -; Genomic_DNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR011134; Netrin C.
DR InterPro; IPR011497; Prot_Inh_Kazal_2.

DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.

Query Match 64.0%; Score 229; DB 2; Length 569;
Best Local Similarity 62.7%; Pred. No. 1.3e-17;
Matches 37; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 GP- GDACVLPAVQPCRGWEPWAYSPLLQCHPFFVYGGCGNGNNFHRSCEDEDACP 57
DB 377 GPLSEPCGLPALQGPCKSEPRWAYSSSLHQCSFYGGCGNGNNFHRSCEACEETCP 435

RESULT 8
Q7TQN3_MOUSE
ID Q7TQN3_MOUSE PRELIMINARY; PRT; 571 AA.
AC Q7TQN3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth and differentiation factor-associated serum protein 1.
DE Name=Wfikn2; Synonyms=Gaspl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX MEDLINE=22656519; PubMed=12595574; DOI=10.1210/me.2002-0366;
RA Hill J.J., Qiu Y., Hewick R.M., Wolfman N.M.;
RT "Regulation of myostatin in vivo by growth and differentiation factor-
RT associated serum protein-1: a novel protein with protease inhibitor
RT and follistatin domains.";
RL Mol. Endocrinol. 17:1144-1154(2003).
DR EMBL; AY308804; AAF72503.1; -; mRNA.
DR HSSP; P00974; 1K09.
DR Ensembl; ENSMUSG000004177; Mus musculus.
DR MGI; MGI:2669209; Wfikn2.
DR GO; GO:0005315; P:protein binding; IPI.
DR GO; GO:0007179; P:transforming growth factor beta receptor si. . .; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_Inh_Kazal_2.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.

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DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00189; NTR; 1.
SQ SEQUENCE 571 AA; 63331 MW; B2BE676B3DC71256 CRC64;

Query Match 63.4%; Score 227; DB 2; Length 571;
Best Local Similarity 62.7%; Pred. No. 2.8e-17;
Matches 37; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GFGDACVLPAVQGPCRGWPRWAYSPLLQQCHPFFVYGGCEGNGNNFHSRSCEDACPVP 59
Db 376 GPLATCSLPALQGPCKAYVPRWAYNSQTGLCSQFVYGGCEGNGNNFHSRSCEDACPVP 434

RESULT 9
Q5US5 MOUSE PRELIMINARY; PRT; 571 AA.
AC Q5US5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein (AY100450) (WFIKN-like growth and differentiation
DE factor-associated serum protein 1) (Gaspl).
GN Name=RP23-244C22.2; ORFNames=RP23-244C22.2-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP Tracey A.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL645846; CA124703.1; -; Genomic DNA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR01134; Netrin C.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00189; NTR; 1.
SQ SEQUENCE 571 AA; 63333 MW; 3A75A449F53703AA CRC64;

Query Match 63.1%; Score 226; DB 2; Length 571;
Best Local Similarity 62.7%; Pred. No. 2.8e-17;
Matches 37; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 GFGDACVLPAVQGPCRGWPRWAYSPLLQQCHPFFVYGGCEGNGNNFHSRSCEDACPVP 59
Db 376 GPLATCSLPALQGPCKAYVPRWAYNSQTGLCSQFVYGGCEGNGNNFHSRSCEDACPVP 434

RESULT 10
Q4SSG7 TETNG PRELIMINARY; PRT; 572 AA.
AC Q4SSG7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 3 SCAF14730, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00023744001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN NUCLEOTIDE SEQUENCE.
RP Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; CAAR01014730; CAG04115.1; -; Genomic DNA.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR01134; Netrin C.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF01759; NTR; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00189; NTR; 1.
FT NON TER 572 572
SQ SEQUENCE 572 AA; 63585 MW; 697E816BFA4B71E1 CRC64;

Query Match 60.3%; Score 216; DB 2; Length 572;
Best Local Similarity 63.0%; Pred. No. 3.9e-16;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 6 CVLPAVQGPCRGWPRWAYSPLLQQCHPFFVYGGCEGNGNNFHSRSCEDACPVP 59
Db 376 GPLATCSLPALQGPCKAYVPRWAYNSQTGLCSQFVYGGCEGNGNNFHSRSCEDACPVP 434

```





RESULT 13  
Q6NUX0 BRARE PRELIMINARY; PRT; 558 AA.  
ID Q6NUX0 BRARE PRELIMINARY; PRT; 558 AA.  
AC Q6NUX0;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE WAP, follietatin/kazal, immunoglobulin, kunitz and netrin domain  
DE containing 1.  
GN Name=zgc:85816;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RG NIH MGC Project;  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC068398; AAH68398.1; -; mRNA.  
DR HSSP; Q16019; 1AAP.  
DR ZFIN; ZDB-GENE-040426-2465; zgc:85816.  
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG.c2.  
DR InterPro; IPR011497; Netrin C.  
DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
DR InterPro; IPR008197; WAP.  
DR Pfam; PF07648; Kazal\_2; 1.  
DR Pfam; PF00014; Kunitz\_BPTI; 2.  
DR Pfam; PF00095; WAP; 1.  
DR PRINTS; PR00003; 4DISULPHORE.  
DR PRINTS; PR00759; BASICPTASE.  
DR ProDom; PD000222; Prot\_inh\_Kunz-m; 2.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00408; IGC2; 1.  
DR SMART; SM00131; KU; 2.  
DR SMART; SM00217; WAP; 1.  
DR PROSITE; PS00317; 4\_DISULFIDE\_CORE; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 2.  
DR PROSITE; PS00835; IG LIKE; 1.  
DR PROSITE; PS0189; NTR; 1.  
SQ SEQUENCE 558 AA; 61154 MW; 12462B3A7DE540EC CRC64;

Query Match

52.5%; Score 188; DB 2; Length 558;

Best Local Similarity 55.8%; Pred. No. 6e-13;  
Matches 29; Conservative 8; Mismatches 15; Indels 0; Gaps 0;  
QY 6 CVLPAVQPCRGWBPWAYSPLOQCHPFPVYGGCGNGNPHSRESCEADCP 57  
DB 371 CSLPAVQPCRHQARWFYNSLTERCEAFLYGGCGNGNPSFGTRRECDACP 422  
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AC Q6NUV7;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Zgc:85816 protein (Fragment).  
GN Name=zgc:85816;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RG NIH MGC Project;  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC068412; AAH68412.1; -; mRNA.  
DR HSSP; Q16019; 1AAP.  
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG.c2.  
DR InterPro; IPR011497; Netrin C.  
DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
DR InterPro; IPR008197; WAP.  
DR Pfam; PF00014; Kunitz\_BPTI; 2.  
DR Pfam; PF00095; WAP; 1.  
DR PRINTS; PR00003; 4DISULPHORE.  
DR ProDom; PD000222; Prot\_inh\_Kunz-m; 2.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00408; IGC2; 1.  
DR SMART; SM00131; KU; 2.  
DR SMART; SM00217; WAP; 1.  
DR PROSITE; PS00317; 4\_DISULFIDE\_CORE; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 2.  
DR PROSITE; PS00835; IG LIKE; 1.  
DR PROSITE; PS0189; NTR; 1.

DR - PROSITE; PS50835; IG LIKE; 1.  
 DR PROSITE; PS50189; NTR; 1.  
 FT NON\_TER 1  
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 Matches 28; Conservative 9; Mismatches 15; Indels 0; Gaps 0;  
 OY 6 CVLPAVQPCRGWPRWYSLPQQCHPVYVGCEGNGNNFHSRSCEDACP 57  
 DB 314 CSLPAVQPCRGWQARWYNSLTERCEAFYLGCGSGNKNSTGTQRCDAHCP 365  
 RESULT 15  
 AMBP\_RAT  
 ID AMBP\_RAT STANDARD; PRT; 349 AA.  
 AC Q64240; P19603; Q63336;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-trypsin inhibitor light chain (IIT-LC) (Bikunin) (HI-30); Trypsin].  
 GN Name=Ambp; Synonyms=Iitl;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Murioidea; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=92182014; PubMed=1371936; DOI=10.1016/0167-4781(92)90462-9; Lindqvist A., Bratt T., Alkieri M., Kasterstroem B.;  
 RA "Rat alpha 1-microglobulin: co-expression in liver with the light chain of inter-alpha-trypsin inhibitor.";  
 RL Biochim. Biophys. Acta 1130:63-67(1992).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Spleen;  
 RG NIH - Mammalian Gene Collection (MGC) project;  
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE OF 141-195.  
 RX MEDLINE=87037744; PubMed=2429963;  
 RA Kasterstroem W., Bjoerck L., Akerstroem B.;  
 RT "Developmental and tissue-specific expression of alpha 1-microglobulin mRNA in the rat.";  
 RL J. Biol. Chem. 261:15070-15074(1986).  
 RN [4]  
 RP PROTEIN SEQUENCE OF 283-343, AND CHARACTERIZATION.  
 RC STRAIN=Wistar;  
 RX MEDLINE=89053978; PubMed=3263966;  
 RA Kido H., Yokogoshi Y., Katunuma N.;  
 RT "Kunitz-type protease inhibitor found in rat mast cells. Purification, properties, and amino acid sequence.";  
 RL J. Biol. Chem. 263:3818-3822(1988).  
 RN [5]  
 RP PROCESSING.  
 RX MEDLINE=94148892; PubMed=7508921;  
 RA Itoh H., Ide H., Ishikawa N., Nawa Y.;  
 RT "Mast cell protease inhibitor, trypsin, is a fragment of inter-alpha-trypsin inhibitor light chain.";  
 RL J. Biol. Chem. 269:3818-3822(1994).  
 RN [6]  
 RP INTERACTION WITH FNI.  
 RX PubMed=7519849;  
 RA Falkenberg C., Enghild J.J., Thogersen I.B., Salvesen G., Akerstroem B.;  
 RT "Isolation and characterization of fibronectin-alpha 1-microglobulin complex in rat plasma.";  
 RL Biochem. J. 301:745-751(1994).  
 CC -!- FUNCTION: Alpha-1-microglobulin occurs in many physiological fluids including plasma, urine, and cerebrospinal fluid. It appears not only as a free monomer but also in complexes with IgA and albumin (By similarity).  
 CC -!- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and urine, inhibits trypsin, plasmin, and lysosomal granulocytic elastase (By similarity).  
 CC -!- FUNCTION: Trypsin is a trypsin inhibitor. It inhibits blood coagulation factor Xa and trypsin about 100-fold more rapidly than porcine pancreatic trypsin and chymase. It is a monomer but is also found in mast cells as a complex with trypsinase.  
 CC -!- SUBUNIT: I-alpha-1 plasma protease inhibitors are assembled from one or two heavy chains (H1, H2 or H3) and one light chain, bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2 and bikunin, inter-alpha-like inhibitor (I-alpha-LI) of H2 and bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin (By similarity). Interacts with FNI.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Synthesized in the liver and secreted in plasma. Trypsin is present in mast cell granules.  
 CC -!- PTM: The precursor is proteolytically processed into two separately functioning proteins.  
 CC -!- PTM: 3-Hydroxykynurenine, an oxidized tryptophan metabolite that is common in biological fluids, reacts with Cys-52, Lys-110, Lys-136, and Lys-148 to form heterogeneous polycyclic chromophores including hydroxanthomatin. The reaction by alpha-1-microglobulin is autocatalytic. The chromophore can react with accessible cysteines forming non-reducible thioether cross-links with other molecules of alpha-1-microglobulin or with other proteins such as Ig alpha-1 chain C region (By similarity).  
 CC -!- PTM: Heavy chains are interlinked with bikunin via a chondroitin 4-sulfate bridge to the their C-terminal aspartate (By similarity).  
 CC -!- SIMILARITY: In the N-terminal section; belongs to the lipocalin family.  
 CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 CC EMBL; S87544; AAB21782.1; -; mRNA.  
 CC EMBL; BC088166; AAH88166.1; -; mRNA.  
 CC EMBL; J03600; AAA41596.1; -; mRNA.  
 CC PIR; S21089; S21089.  
 CC HSSP; P02760; 1BIK.  
 CC SMR; Q64240; 229-338.  
 CC Ensembl; ENSRNOG0000006889; Rattus norvegicus.  
 CC RGD; 2102; Ambp.  
 CC GO; GO:0005576; C:extracellular region; ISS.  
 CC GO; GO:0005792; C:microsome; IDA.  
 CC GO; GO:0005886; C:plasma membrane; ISS.  
 CC GO; GO:0019855; F:calcium channel inhibitor activity; ISS.  
 CC GO; GO:0046904; F:calcium oxalate binding; ISS.  
 CC GO; GO:0020037; F:heme binding; ISS.  
 CC GO; GO:0019882; F:IgA binding; ISS.  
 CC GO; GO:0030568; F:plasmin inhibitor activity; ISS.  
 CC GO; GO:0042803; F:protein homodimerization activity; ISS.  
 CC GO; GO:0030304; F:trypsin inhibitor activity; ISS.  
 CC GO; GO:0030236; P:anti-inflammatory response; ISS.  
 CC GO; GO:0007155; P:cell adhesion; ISS.  
 CC GO; GO:0042167; P:heme catabolism; ISS.  
 CC GO; GO:0050777; P:negative regulation of immune response; ISS.  
 CC GO; GO:0046329; P:negative regulation of JNK cascade; ISS.  
 CC GO; GO:0007565; P:pregnancy; ISS.  
 CC InterPro; IPR02968; AI-microglobln.  
 CC InterPro; IPR012674; Calycin.  
 CC InterPro; IPR002345; Lipocalin.  
 CC InterPro; IPR000566; Lipocaln\_cytFABP.  
 CC InterPro; IPR002223; Prot\_inh\_Kunz-m.  
 CC Pfam; PF00014; Kunitz\_BPTI; 2.  
 CC Pfam; PF00061; Lipocalin; 1.

DR PRINTS; PRO1215; ALMCGLOBULIN.  
DR PRINTS; PRO0759; BASICPTASE.  
DR PRINTS; PRO0179; LIPOCALIN.  
DR ProDom; PD000222; Prot\_Inh\_Kunz-m; 2.  
DR SMART; SM00131; KU; 2.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 2.  
DR PROSITE; PS00213; LIPOCALIN; 1.  
KW Chromophore; Direct protein sequencing; Glycoprotein; Lipocalin;  
KW Plasma; Protease inhibitor; Repeat; Serine protease inhibitor; Signal.  
FT SIGNAL 1 19 By similarity.  
FT CHAIN 20 202 Alpha-1-microglobulin.  
FT CHAIN 205 349 Inter-alpha-trypsin inhibitor light chain.  
FT CHAIN 283 343 Trypsatin.  
FT DOMAIN 230 280 BPTI/Kunitz inhibitor 1.  
FT DOMAIN 286 336 BPTI/Kunitz inhibitor 2.  
FT BINDING 52 52 Multimeric 3-hydroxykynurenine chromophore (covalent) (By similarity).  
FT BINDING 110 110 Multimeric 3-hydroxykynurenine chromophore (covalent) (By similarity).  
FT BINDING 136 136 Multimeric 3-hydroxykynurenine chromophore (covalent) (By similarity).  
FT BINDING 148 148 Multimeric 3-hydroxykynurenine chromophore (covalent) (By similarity).  
FT SITE 240 241 chromophore (covalent) (By similarity).  
FT SITE 296 297 Inhibitory (P1) (chymotrypsin, elastase) (By similarity).  
FT CARBOHYD 114 114 Inhibitory (P1) (trypsin) (By similarity).  
FT CARBOHYD 233 233 N-linked (GlcNAc . .) (Potential).  
FT DISULFID 90 187 N-linked (GlcNAc . .) (Potential).  
FT DISULFID 230 280 By similarity.  
FT DISULFID 239 263 By similarity.  
FT DISULFID 255 276 By similarity.  
FT DISULFID 286 336 By similarity.  
FT DISULFID 295 319 By similarity.  
FT DISULFID 311 332 By similarity.  
FT CONFLICT 142 142 G -> A (in Ref. 3).  
FT CONFLICT 302 302 W -> L (in Ref. 4).  
FT CONFLICT 323 323 G -> N (in Ref. 4).  
FT CONFLICT 330 331 KE -> PK (in Ref. 4).  
FT CONFLICT 334 334 E -> W (in Ref. 4).  
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Query Match 48.6%; Score 174; DB 1; Length 349;  
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Matches 28; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Qy 5 ACVLPVQGPCRGWEPRWYSPLLQQCHPFPVYGGCGNGNPNFHSRSCEDACPVP 59  
Db 285 ACNLPVQGPCRPAELWAFDAAGKCIQFTYGGCKGNGKPFYSEKCEKCYGVP 339

Search completed: February 16, 2006, 18:33:22  
Job time : 234 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 18:33:37 ; Search time 47 Seconds  
(without alignments)  
103.784 Million cell updates/sec

Title: US-10-021-963-2  
Perfect score: 358  
Sequence: 1 GPGDACLPAVQGPCRGWEP.....EGNGNPHRSRSCDACPVP 59

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5-COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/6-COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H-COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCUTUS-COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE-COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	358	100.0	59	2	US-09-388-183-2
2	172	48.0	56	1	US-08-358-160-20
3	172	48.0	141	1	US-08-358-160-69
4	170	47.5	56	1	US-08-358-160-19
5	170	47.5	58	2	US-08-676-124-132
6	170	47.5	58	2	US-09-414-878-132
7	170	47.5	58	2	US-09-240-136-132
8	170	47.5	58	2	US-09-638-770A-132
9	170	47.5	58	2	US-10-167-351-132
10	170	47.5	65	1	US-08-358-160-152
11	170	47.5	122	6	US-08-422-333-12
12	170	47.5	122	6	5187153-20
13	170	47.5	122	6	5220013-23
14	170	47.5	122	6	5223482-22
15	170	47.5	122	6	5466783-23
16	170	47.5	141	1	US-08-358-160-67
17	169	47.2	66	1	US-08-358-160-113
18	169	47.2	79	6	5466783-7
19	167.5	46.8	62	1	US-08-358-160-97
20	166	46.4	58	1	US-08-676-125A-49
21	166	46.4	58	1	US-09-136-012A-49
22	166	46.4	65	1	US-08-358-160-149
23	166	46.4	123	6	5466783-22
24	165	46.1	58	2	US-08-676-124-133
25	165	46.1	58	2	US-09-414-878-133
26	165	46.1	58	2	US-09-240-136-133
27	165	46.1	58	2	US-09-638-770A-133

28	165	46.1	58	2	US-10-167-351-133	Sequence 133, App
29	165	46.1	65	1	US-08-358-160-127	Sequence 127, App
30	165	46.1	65	1	US-08-358-160-133	Sequence 133, App
31	165	46.1	123	6	5466783-21	Patent No. 5466783
32	164	45.8	58	1	US-08-358-160-71	Sequence 71, Appl
33	164	45.8	58	2	US-08-676-124-71	Sequence 71, Appl
34	164	45.8	58	2	US-08-676-124-131	Sequence 131, App
35	164	45.8	58	2	US-09-414-878-71	Sequence 71, Appl
36	164	45.8	58	2	US-09-414-878-131	Sequence 131, App
37	164	45.8	58	2	US-09-240-136-71	Sequence 71, Appl
38	164	45.8	58	2	US-09-240-136-131	Sequence 131, App
39	164	45.8	58	2	US-09-638-770A-71	Sequence 71, Appl
40	164	45.8	58	2	US-09-638-770A-131	Sequence 131, App
41	164	45.8	58	2	US-10-167-351-71	Sequence 71, Appl
42	164	45.8	58	2	US-10-167-351-131	Sequence 131, App
43	164	45.8	68	1	US-07-972-387-37	Sequence 37, Appl
44	164	45.8	68	1	US-08-431-412-37	Sequence 37, Appl
45	164	45.8	68	1	US-08-057-971-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1  
US-09-388-183-2  
; Sequence 2, Application US/09388183  
; Patent No. 6380354  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN6  
; FILE REFERENCE: 98-40  
; CURRENT APPLICATION NUMBER: US/09/388.183  
; CURRENT FILING DATE: 1999-09-01  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 59  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-388-183-2

Query Match 100.0%; Score 358; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 7.5e-35;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGDACLPAVQGPCRGWEPWAYSPILQQCHPFFVYGCNGNPHRSRSCDACPVP 59  
Db 1 GPGDACLPAVQGPCRGWEPWAYSPILQQCHPFFVYGCNGNPHRSRSCDACPVP 59  
|||||

RESULT 2  
US-08-358-160-20  
; Sequence 20, Application US/08358160  
; Patent No. 5663143  
; GENERAL INFORMATION:  
; APPLICANT: LEY, Arthur C.  
; APPLICANT: LADNER, Robert C.  
; APPLICANT: GUTERMAN, Sonia K.  
; APPLICANT: ROBERTS, Bruce L.  
; APPLICANT: MARKLAND, William  
; APPLICANT: KENT, Rachel B.  
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ  
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE  
; NUMBER OF SEQUENCES: 234  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W. Suite 300  
; CITY: Washington  
; STATE: District of Columbia  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM: Floppy disk  
; MEDIUM TYPE: Floppy disk

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; - COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-20

Query Match      48.0%; Score 172; DB 1; Length 56;
Best Local Similarity 50.0%; Pred. No. 4.2e-13;
Matches 28; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Qy      4 DACTVPAVGPCRGWEPRWAYSPLLQQCHPFFVYGCGEGNGNNHRSRSCEDACPV 59
       :|||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      1 EACNLPVIRGPCIAFPFRWAFDAVKGKCVLPFYGGCQGNGNKFYSEKECYCGVP 56

RESULT 3
US-08-358-160-69
; Sequence 69, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-69

Query Match      48.0%; Score 172; DB 1; Length 56;
Best Local Similarity 50.0%; Pred. No. 4.2e-13;
Matches 28; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Qy      4 DACTVPAVGPCRGWEPRWAYSPLLQQCHPFFVYGCGEGNGNNHRSRSCEDACPV 59
       :|||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      1 EACNLPVIRGPCIAFPFRWAFDAVKGKCVLPFYGGCQGNGNKFYSEKECYCGVP 56

RESULT 4
US-08-358-160-19
; Sequence 19, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-69

Query Match      48.0%; Score 172; DB 1; Length 141;
Best Local Similarity 50.0%; Pred. No. 1.1e-12;
Matches 28; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Qy      4 DACTVPAVGPCRGWEPRWAYSPLLQQCHPFFVYGCGEGNGNNHRSRSCEDACPV 59
       :|||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      86 EACNLPVIRGPCIAFPFRWAFDAVKGKCVLPFYGGCQGNGNKFYSEKECYCGVP 141

RESULT 4
US-08-358-160-19
; Sequence 19, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-69

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5

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P R I O R   A P P L I C A T I O N   D A T A :
A P P L I C A T I O N   N U M B E R :    09 / 240 , 136
F I L I N G   D A T E :    29 - J A N - 1999
P R I O R   A P P L I C A T I O N   D A T A :
A P P L I C A T I O N   N U M B E R :    08 / 676 , 124
F I L I N G   D A T E :    07 - J A N - 1997
P R I O R   A P P L I C A T I O N   D A T A :
A P P L I C A T I O N   N U M B E R :    P C T / U S 95 / 00298
F I L I N G   D A T E :    11 - J A N - 1995
P R I O R   A P P L I C A T I O N   D A T A :
A P P L I C A T I O N   N U M B E R :    08 / 208 , 265
F I L I N G   D A T E :    10 - M A R - 1994
P R I O R   A P P L I C A T I O N   D A T A :
A P P L I C A T I O N   N U M B E R :    08 / 179 , 685
F I L I N G   D A T E :    11 - J A N - 1994

```

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;
;
; * ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-414-878-132

Query Match          47.5%; Score 170; DB 2; Length 58;
Best Local Similarity 52.7%; Pred. No. 7.5e-13;
Matches 29; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 5 ACVLPAVGQPCRGWEPWAYSPLLQQCHPFFVYGGCEGNGNHFHSRSCEDACVPV 59
   ||||| ||||| ||||| : : ||||| ||||| : : |||||
Db 4 ACNLPVTGPCRRARFORWAFDAVKGCVLFFVYGGCGNGNKFYSEKREYCGVP 58

RESULT 7
US-09-240-136-132
; Sequence 132, Application US/09240136
; Patent No. 6103499
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; FROM THE KUNITZ DOMAINS
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,136
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-8801
; TELEFAX: 617-491-4343
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-638-770A-132
```

```
;
;
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-240-136-132

Query Match          47.5%; Score 170; DB 2; Length 58;
Best Local Similarity 52.7%; Pred. No. 7.5e-13;
Matches 29; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 5 ACVLPAVGQPCRGWEPWAYSPLLQQCHPFFVYGGCEGNGNHFHSRSCEDACVPV 59
   ||||| ||||| ||||| : : ||||| ||||| : : |||||
Db 4 ACNLPVTGPCRRARFORWAFDAVKGCVLFFVYGGCGNGNKFYSEKREYCGVP 58

RESULT 8
US-09-638-770A-132
; Sequence 132, Application US/09638770A
; Patent No. 6423498
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plamin Derived
; FROM THE KUNITZ DOMAINS
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,770A
; FILING DATE: 15-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-8801
; TELEFAX: 617-491-4343
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-638-770A-132
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Query Match      47.5%; Score 170; DB 2; Length 58;
Best Local Similarity 52.7%; Pred. No. 7.5e-13;
Matches 29; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 5 ACVLPAVQGPCRGWEPRWAYSPLLQOCHPFVYGGCEGNGNHFHRSCEDEDACPV 59
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 ACNLPVTGPCRRARFORWAFDAVKGKCVLFVYGGCGNGNKFYSKECKEYCGVP 58
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-10-167-351-132
; Sequence 132, Application US/10167351
; Patent No. 6953674
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: LADNER, Robert C.
; APPLICANT: Markland, William
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
; FILE REFERENCE: DYX-007.2P US-4
; CURRENT APPLICATION NUMBER: US/10/167,351
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 09/638,770
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 09/414,878
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 09/240,136
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 08/676,124
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: PCT/US95/00298
; PRIOR FILING DATE: 1995-01-11
; PRIOR APPLICATION NUMBER: 08/208,265
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: 08/179,658
; PRIOR FILING DATE: 1994-01-11
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 132
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: design plasmin inhibitors
US-10-167-351-132

Query Match      47.5%; Score 170; DB 2; Length 59;
Best Local Similarity 52.7%; Pred. No. 7.5e-13;
Matches 29; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 5 ACVLPAVQGPCRGWEPRWAYSPLLQOCHPFVYGGCEGNGNHFHRSCEDEDACPV 59
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 ACNLPVTGPCRRARFORWAFDAVKGKCVLFVYGGCGNGNKFYSKECKEYCGVP 58
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-08-358-160-152
; Sequence 152, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia

```

```

; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 152:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-152

Query Match      47.5%; Score 170; DB 1; Length 65;
Best Local Similarity 48.2%; Pred. No. 8.4e-13;
Matches 27; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 4 DACVLPAVQGPCRGWEPRWAYSPLLQOCHPFVYGGCEGNGNHFHRSCEDEDACPV 59
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 EACNLPVQGPCRAFIOLWAFDAVKGKCVRFSGCKGNGNKFYSQKECKEYCGIP 59
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RESULT 11
US-08-422-333-12
; Sequence 12, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30

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* CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,333
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Shearer, Peter R.
; REGISTRATION NUMBER: 28,117
; REFERENCE/DOCKET NUMBER: 21900-28048.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 966-1550
; FAX: (415) 968-2438
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-422-333-12

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Best Local Similarity 48.2%; Pred. No. 1.7e-12;
Matches 27; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

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Db 59 EACNLPVQGPCRAFIQLWAFDAVKGKCVRFSGYGGCKGNKGFYSQKECKEYCGIP 114

RESULT 12
5187153-20
;Patent No. 5187153
;APPLICANT: CORDELL, BARBARA;SCHILLING, JAMES W.;KATUNUMA, NOBUHIKO
;TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
;AMYLOID POLYPEPTIDE DERIVATIVES
;NUMBER OF SEQUENCES: 33
;CURRENT APPLICATION DATA:
; FILING DATE: 29-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 361,912
; FILING DATE: 06-JUN-1989
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
;SEQ ID NO:20:
; LENGTH: 122
5187153-20

Query Match          47.5%; Score 170; DB 6; Length 122;
Best Local Similarity 48.2%; Pred. No. 1.7e-12;
Matches 27; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 4 DACVLPAVQGPCRGWEPRWAYSPLLQOCHPFVYGGCEGNGNHFHSRSCEDACVPV 59
Db 59 EACNLPVQGPCRAFIQLWAFDAVKGKCVRFSGYGGCKGNKGFYSQKECKEYCGIP 114

RESULT 13
5220013-23
;Patent No. 5220013
;APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
;TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
;OF ALZHEIMER'S DISEASE
;NUMBER OF SEQUENCES: 30
;CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 23-NOV-1987

* CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,333
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Shearer, Peter R.
; REGISTRATION NUMBER: 28,117
; REFERENCE/DOCKET NUMBER: 21900-28048.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 966-1550
; FAX: (415) 968-2438
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-422-333-12

Query Match          47.5%; Score 170; DB 6; Length 122;
Best Local Similarity 48.2%; Pred. No. 1.7e-12;
Matches 27; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 4 DACVLPAVQGPCRGWEPRWAYSPLLQOCHPFVYGGCEGNGNHFHSRSCEDACVPV 59
Db 59 EACNLPVQGPCRAFIQLWAFDAVKGKCVRFSGYGGCKGNKGFYSQKECKEYCGIP 114

RESULT 14
5223482-22
;Patent No. 5223482
;APPLICANT: SCHILLING, JAMES W.;PONTE, PHYLLIS A.;CORDELL,
;BARBARA
;TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
;INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
;NUMBER OF SEQUENCES: 34
;CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/361,912
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
;SEQ ID NO:22:
; LENGTH: 122
5223482-22

Query Match          47.5%; Score 170; DB 6; Length 122;
Best Local Similarity 48.2%; Pred. No. 1.7e-12;
Matches 27; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 4 DACVLPAVQGPCRGWEPRWAYSPLLQOCHPFVYGGCEGNGNHFHSRSCEDACVPV 59
Db 61 EACNLPVQGPCRAFIQLWAFDAVKGKCVRFSGYGGCKGNKGFYSQKECKEYCGIP 116

RESULT 15
5466783-23
;Patent No. 5466783
;APPLICANT: Wun, Tze-Chien;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
;TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
;NUMBER OF SEQUENCES: 26
;CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
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APPLICATION NUMBER: 77,366  
FILING DATE: 23-JUL-1987  
SEQ ID NO:23:  
LENGTH: 122  
5466783-23  
Query Match 47.5%; Score 170; DB 6; Length 122;  
Best Local Similarity 48.2%; Pred. No. 1.7e-12;  
Matches 27; Conservative 12; Mismatches 17; Indels 0; Gaps 0;  
Oy 4 DACVLPVQGPCRCGWEPRWAYSPLLQOCHPFVYGGCEGNGNPHSRSCEDACPVP 59  
Db 58 EACNLPVQGPCRAPIQLWAFDAVKGCVRFSYGGCKGNGNKFYQKECKEYCGIP 113

Search completed: February 16, 2006, 18:34:58  
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 18:44:52 ; Search time 166 Seconds  
(without alignments)  
148.506 Million cell updates/sec

Title: US-10-021-963-2

Perfect score: 358  
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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
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5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	358	100.0	59	4	US-10-021-963-2
2	358	100.0	491	4	US-10-029-386-33637
3	358	100.0	548	3	US-09-819-136-2
4	358	100.0	548	4	US-10-239-663-47
5	358	100.0	548	4	US-10-369-736-11
6	358	100.0	548	4	US-10-369-738-11
7	358	100.0	548	6	US-11-028-058-11
8	323	90.2	552	4	US-10-369-736-9
9	323	90.2	552	4	US-10-369-738-9
10	323	90.2	552	6	US-11-028-058-9
11	239	66.8	503	4	US-10-007-280A-233
12	239	66.8	576	3	US-09-794-589-2
13	239	66.8	576	4	US-10-315-380-2
14	239	66.8	576	4	US-10-369-736-7
15	239	66.8	576	4	US-10-369-738-7
16	239	66.8	576	6	US-11-028-058-7
17	239	66.8	640	4	US-10-369-736-5
18	239	66.8	640	4	US-10-369-738-5
19	239	66.8	640	6	US-11-028-058-5
20	227	63.4	571	4	US-10-369-736-3
21	227	63.4	571	4	US-10-369-736-49
22	227	63.4	571	4	US-10-369-738-3
23	227	63.4	571	4	US-10-369-738-49
24	227	63.4	571	6	US-11-028-058-3
25	227	63.4	571	6	US-11-028-058-49
26	178	49.7	655	4	US-10-361-997-61
27	178	49.7	655	5	US-10-503-834-61

28	178	49.7	728	4	US-10-361-997-75	Sequence 75, Appl
29	178	49.7	728	5	US-10-503-834-80	Sequence 80, Appl
30	178	49.7	729	4	US-10-361-997-46	Sequence 46, Appl
31	178	49.7	729	5	US-10-503-834-46	Sequence 46, Appl
32	178	49.7	752	4	US-10-361-997-74	Sequence 74, Appl
33	178	49.7	752	5	US-10-503-834-79	Sequence 79, Appl
34	178	49.7	753	4	US-10-361-997-45	Sequence 45, Appl
35	178	49.7	753	5	US-10-503-834-45	Sequence 45, Appl
36	172	48.0	56	4	US-10-038-722-27	Sequence 27, Appl
37	172	48.0	56	4	US-10-456-986A-49	Sequence 49, Appl
38	172	48.0	56	4	US-10-361-997-40	Sequence 40, Appl
39	172	48.0	56	5	US-10-931-153-23	Sequence 23, Appl
40	172	48.0	56	5	US-10-953-902A-49	Sequence 49, Appl
41	172	48.0	56	5	US-10-503-834-20	Sequence 20, Appl
42	172	48.0	141	4	US-10-038-722-74	Sequence 74, Appl
43	172	48.0	655	4	US-10-361-997-59	Sequence 59, Appl
44	172	48.0	655	5	US-10-503-834-59	Sequence 59, Appl
45	172	48.0	694	4	US-10-361-997-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1  
US-10-021-963-2  
; Sequence 2, Application US/10021963  
; Publication No. US20020110887A1  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN6  
; FILE REFERENCE: 98-40  
; CURRENT APPLICATION NUMBER: US/10/021,963  
; CURRENT FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US/09/388,183  
; PRIOR FILING DATE: 1999-09-01  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 59  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-021-963-2

Query Match 100.0%; Score 358; DB 4; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.1e-32;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GPGDACLPAVQPCRGWEPWYSPLLQCHPPFYVGGCGNGNNFHRSCEADACVP 59
Db	1	GPGDACLPAVQPCRGWEPWYSPLLQCHPPFYVGGCGNGNNFHRSCEADACVP 59

RESULT 2  
US-10-029-386-33637  
; Sequence 33637, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: AEMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 33637  
; LENGTH: 491  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO 284479.1

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; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: SWISSPROT HIT: Q62577, EVALUE 4.00e-17
US-10-029-386-33637

Query Match      100.0%; Score 358; DB 4; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.6e-31;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-819-136-2
; Sequence 2, Application US/09819136
; Patent No. US20020146789A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; TITLE OF INVENTION: MULTI-DOMAIN PROTEINASE INHIBITOR
; FILE REFERENCE: 00-25
; CURRENT APPLICATION NUMBER: US/09/819,136
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/193,642
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-136-2

Query Match      100.0%; Score 358; DB 3; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGDACVLPVQVQPCRGWEPRWAYSPLLQQCHPFPVYGGCEGNGNNFHSRSCEDACPVP 59
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RESULT 4
US-10-239-663-47
; Sequence 47, Application US/10239663
; Publication No. US20030139572A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/10/239,663
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-239-663-47
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Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 354 GPGDACVLPVQVQPCRGWEPRWAYSPLLQQCHPFPVYGGCEGNGNNFHSRSCEDACPVP 412

RESULT 5
US-10-369-736-11
; Sequence 11, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-736-11

Query Match      100.0%; Score 358; DB 4; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGDACVLPVQVQPCRGWEPRWAYSPLLQQCHPFPVYGGCEGNGNNFHSRSCEDACPVP 59
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Db 354 GPGDACVLPVQVQPCRGWEPRWAYSPLLQQCHPFPVYGGCEGNGNNFHSRSCEDACPVP 412

RESULT 6
US-10-369-738-11
; Sequence 11, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-738-11

Query Match      100.0%; Score 358; DB 4; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGDACVLPVQVQPCRGWEPRWAYSPLLQQCHPFPVYGGCEGNGNNFHSRSCEDACPVP 59
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Db 354 GPGDACVLPVQVQPCRGWEPRWAYSPLLQQCHPFPVYGGCEGNGNNFHSRSCEDACPVP 412
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; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,640
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 233
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-007-280A-233

Query Match      66.8%; Score 239; DB 4; Length 503;
Best Local Similarity 66.1%; Pred. No. 3.e-18;
Matches 39; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

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RESULT 12
US-09-794-589-2
; Sequence 2, Application US/09794589
; Patent No. US20020004224A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/09/794,589
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-589-2

Query Match      66.8%; Score 239; DB 3; Length 576;
Best Local Similarity 66.1%; Pred. No. 3.4e-18;
Matches 39; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

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Db 381 GPLAACSLPALQGPCKAYAPRWAYNSQTGCQSFVYGGCEGNGNHFHSRSCPP 439

RESULT 13
US-10-315-380-2
; Sequence 2, Application US/10315380
; Publication No. US20030129577A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/10/315,380
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/794,589
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-315-380-2

Query Match      66.8%; Score 239; DB 4; Length 576;
Best Local Similarity 66.1%; Pred. No. 3.4e-18;
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Matches 39; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

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Db 381 GPLAACSLPALQGPCKAYAPRWAYNSQTGCQSFVYGGCEGNGNHFHSRSCPP 439

RESULT 14
US-10-369-736-7
; Sequence 7, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-736-7

Query Match      66.8%; Score 239; DB 4; Length 576;
Best Local Similarity 66.1%; Pred. No. 3.4e-18;
Matches 39; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GPGDACVLPAVQGPCRGWEPRWAYSPLLQQCHPFFVYGGCEGNGNHFHSRSCEDACVP 59
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 381 GPLAACSLPALQGPCKAYAPRWAYNSQTGCQSFVYGGCEGNGNHFHSRSCPP 439

RESULT 15
US-10-369-738-7
; Sequence 7, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-738-7

Query Match      66.8%; Score 239; DB 4; Length 576;
Best Local Similarity 66.1%; Pred. No. 3.4e-18;
Matches 39; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GPGDACVLPAVQGPCRGWEPRWAYSPLLQQCHPFFVYGGCEGNGNHFHSRSCEDACVP 59
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 381 GPLAACSLPALQGPCKAYAPRWAYNSQTGCQSFVYGGCEGNGNHFHSRSCPP 439

Search completed: February 16, 2006, 18:48:04
Job time : 167 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 18:45:27 ; Search time 17 Seconds  
(without alignments)  
49.333 Million cell updates/sec

Title: US-10-021-963-2

Perfect score: 358  
Sequence: 1 GPGDACLPAVQGPCRGWEP.....BGNNGNPHSRSCEDACPVP 59

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA New:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*  
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8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	358	100.0	548	7	US-11-137-465-47 Sequence 47, Appl
2	163	45.5	213	7	US-11-183-555-6 Sequence 6, Appl
3	163	45.5	235	6	US-10-821-234-1398 Sequence 1398, Ap
4	163	45.5	352	7	US-11-000-463-450 Sequence 450, App
5	163	45.5	352	7	US-11-000-463-922 Sequence 922, App
6	163	45.5	352	7	US-11-177-506-28 Sequence 28, Appl
7	138.5	38.7	94	6	US-10-821-234-1123 Sequence 1123, Ap
8	138	38.5	276	7	US-11-183-555-5 Sequence 5, Appl
9	138	38.5	304	6	US-10-821-234-1540 Sequence 1540, Ap
10	132.5	37.0	763	6	US-10-821-234-1519 Sequence 1519, Ap
11	128	35.8	770	6	US-10-982-545-15 Sequence 15, Appl
12	128	35.8	770	6	US-10-789-273-38 Sequence 38, Appl
13	118	33.0	58	7	US-11-068-783-54 Sequence 54, Appl
14	107.5	30.0	353	7	US-11-137-465-44 Sequence 44, Appl
15	107.5	30.0	448	7	US-11-137-465-45 Sequence 45, Appl
16	91	25.4	99	5	US-09-978-360A-492 Sequence 492, App
17	81	22.6	99	5	US-09-978-360A-618 Sequence 618, App
18	70	19.6	830	6	US-10-995-561-899 Sequence 899, App
19	67	18.7	400	7	US-11-077-386-24 Sequence 24, Appl
20	67	18.7	400	7	US-11-077-386-26 Sequence 26, Appl
21	67	18.7	534	7	US-11-077-386-25 Sequence 25, Appl
22	67	18.7	1342	6	US-10-770-726-63 Sequence 63, Appl
23	67	18.7	1342	6	US-11-113-202-12 Sequence 12, Appl
24	67	18.7	1342	7	US-11-113-202-14 Sequence 14, Appl
25	66.5	18.6	1477	7	US-11-149-003-8 Sequence 8, Appl

26	66.5	18.6	1512	7	US-11-149-003-10 Sequence 10, Appl
27	66.5	18.6	1535	7	US-11-149-003-14 Sequence 14, Appl
28	66.5	18.6	1570	7	US-11-149-003-12 Sequence 12, Appl
29	66.5	18.6	1593	7	US-11-149-003-4 Sequence 4, Appl
30	66.5	18.6	1628	7	US-11-149-003-2 Sequence 2, Appl
31	64.5	18.0	5405	7	US-11-108-172-1116 Sequence 1116, Ap
32	63.5	17.7	1342	7	US-11-149-003-24 Sequence 24, Appl
33	61	17.0	1210	7	US-11-113-202-6 Sequence 6, Appl
34	61	17.0	1210	7	US-11-145-566-1 Sequence 1, Appl
35	60.5	16.9	969	6	US-10-055-877-214 Sequence 214, App
36	59.5	16.6	638	7	US-11-054-281-115 Sequence 115, App
37	59	16.3	1158	7	US-11-075-646-6 Sequence 6, Appl
38	58.5	16.3	334	7	US-11-055-822-980 Sequence 980, App
39	57	15.9	1185	6	US-10-877-346-7 Sequence 7, Appl
40	57	15.9	1418	6	US-10-453-372-864 Sequence 864, App
41	57	15.9	1450	6	US-10-055-877-48 Sequence 48, Appl
42	57	15.9	1450	6	US-10-453-372-874 Sequence 874, App
43	56.5	15.8	353	7	US-11-182-592-6 Sequence 6, Appl
44	56.5	15.8	353	7	US-11-182-592-4 Sequence 4, Appl
45	56.5	15.8	604	6	US-10-453-372-1160 Sequence 1160, Ap

## ALIGNMENTS

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RESULT 1
US-11-137-465-47
; Sequence 47, Application US/11137465
; Publication No. US2005025558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GFS0018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-47

Query Match      100.0%; Score 358; DB 7; Length 548;
Best Local Similarity 100.0%; Pred. No. 7.9e-34;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 GPGDACLPAVQGPCRGWEPRLAQCGPFYGGCEGNGNPHSRSCEDACPVP 59
Db      354 GPGDACLPAVQGPCRGWEPRLAQCGPFYGGCEGNGNPHSRSCEDACPVP 412

RESULT 2
US-11-183-555-6
; Sequence 6, Application US/11183555
; Publication No. US20060025329A1
; GENERAL INFORMATION:
; APPLICANT: Hembrough, Todd

```

APPLICANT: Papathanassiou, Adonia E.  
APPLICANT: Green, Shawn J.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation  
TITLE OF INVENTION: Comprising TPR1 Fragments  
FILE REFERENCE: 05213-0297 (43170-300210)  
CURRENT FILING DATE: 2005-07-18  
CURRENT APPLICATION NUMBER: US/11/183,555  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: US 09/766,778  
PRIOR FILING DATE: 1999-01-11  
PRIOR APPLICATION NUMBER: US 08/796,850  
PRIOR FILING DATE: 1997-02-06  
PRIOR APPLICATION NUMBER: US 09/130,273  
PRIOR FILING DATE: 1998-08-06  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 6  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide  
US-11-183-555-6

Query Match 45.5%; Score 163; DB 7; Length 213;  
Best Local Similarity 50.9%; Pred. No. 6,6e-12;  
Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 4 DACVLPAVQPCRGWEPFRWYSPLLQCHPFYVGGCEGNGNPFHSRSCEDAC 56  
Db 12 EICLLPLDYGCRCALLRLRYYYDRYQSCRFYVGGCEGNGNPFYWEACDDAC 64

RESULT 3  
US-10-821-234-1398  
Sequence 1398, Application US/10821234  
Publication No. US20050255114A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Birgit  
APPLICANT: Andarmani, Susan  
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preclampsia  
FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234  
CURRENT FILING DATE: 2004-04-07  
PRIOR APPLICATION NUMBER: US 60/462,047  
PRIOR FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704  
SOFTWARE: pt SEQ\_genes Version 1.0  
SEQ ID NO 1398  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-821-234-1398

Query Match 45.5%; Score 163; DB 6; Length 235;  
Best Local Similarity 50.9%; Pred. No. 7,2e-12;  
Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 4 DACVLPAVQPCRGWEPFRWYSPLLQCHPFYVGGCEGNGNPFHSRSCEDAC 56  
Db 34 EICLLPLDYGCRCALLRLRYYYDRYQSCRFYVGGCEGNGNPFYWEACDDAC 86

RESULT 4  
US-11-000-463-450  
Sequence 450, Application US/11000463  
Publication No. US20050266423A1  
GENERAL INFORMATION:  
APPLICANT: Tang, Y Tom  
APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod  
APPLICANT: Chen, Rui-hong  
APPLICANT: Qian, Xiaohong B.  
APPLICANT: Wang, Zhiwei  
APPLICANT: Wehrman, Tom  
APPLICANT: Zhang, Jie  
APPLICANT: Zhou, Ping  
APPLICANT: Cao, Yi-Cheng  
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
FILE REFERENCE: 785CIPACN  
CURRENT APPLICATION NUMBER: US/11/000,463  
CURRENT FILING DATE: 2004-11-29  
PRIOR APPLICATION NUMBER: 10/291,265  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: PCT/US01/02623  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 09/922,279  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: 09/491,404  
PRIOR FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: 09/617,746  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 09/631,451  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 09/633,870  
PRIOR FILING DATE: 2000-09-15  
NUMBER OF SEQ ID NOS: 944  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 450  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-000-463-450

Query Match 45.5%; Score 163; DB 7; Length 352;  
Best Local Similarity 49.1%; Pred. No. 1e-11;  
Matches 27; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Qy 5 ACVLPAVQPCRGWEPFRWYSPLLQCHPFYVGGCEGNGNPFHSRSCEDACPVY 59  
Db 286 ACNPLPYGFCRAPIQLMAFDVAGKCVLPFYVGGCEGNGNPFYSEKREHYCGPV 340

RESULT 5  
US-11-000-463-922  
Sequence 922, Application US/11000463  
Publication No. US20050266423A1  
GENERAL INFORMATION:  
APPLICANT: Tang, Y Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Chen, Rui-hong  
APPLICANT: Qian, Xiaohong B.  
APPLICANT: Wang, Zhiwei  
APPLICANT: Wehrman, Tom  
APPLICANT: Zhang, Jie  
APPLICANT: Zhou, Ping  
APPLICANT: Cao, Yi-Cheng  
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
FILE REFERENCE: 785CIPACN  
CURRENT APPLICATION NUMBER: US/11/000,463  
CURRENT FILING DATE: 2004-11-29  
PRIOR APPLICATION NUMBER: 10/291,265  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: PCT/US01/02623  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 09/922,279  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: 09/491,404  
PRIOR FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: 09/617,746

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; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 922
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-922

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Query Match 45.5%; Score 163; DB 7; Length 352;  
Best Local Similarity 49.1%; Pred. No. 1e-11;  
Matches 27; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

**Qy**            5 ACVLPAVQGRCRGEPRWAYSPLLLQQCHPFYVGCGEGNNPHSRSESCDACPVP 59  
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
**Db**         286 ACNLTIVRGPCRAFIOLWAFDAVKGKCVLFPYGGCOGNKNKFYEKECEYCGVP 340  
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RESULT 6
US-11-177-506-28
; Sequence 28, Application US/11177506
; Publication No. US20060029956A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Wayne F.
; APPLICANT: Venetta, Thomas M.
; APPLICANT: Groelke, John W.
; APPLICANT: Blasius, Rainer H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF OVARIAN DISEASE
; FILE REFERENCE: 46143/294851
; CURRENT APPLICATION NUMBER: US/11/177,506
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: 60/586,856
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-177-506-28

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Query Match      45.5%; Score 163; DB 7; Length 352;
Best Local Similarity 49.1%; Pred. No. 1e-11;
Matches 27; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
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**Qy**

5 ACVLPAVQPGRGWEPWAYSPLLQQCHPFYVGCEGNGNPHSRSESCDACPVP 59  
||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

**D6**

286 ACNLPTVRGPCCAFIOIWAFDAVKGGKCVLFPYGCGGNKNKFSEKECREYCGRP 340  
||||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

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RESULT 7
US-10-821-234-1123
; Sequence 1123, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1123

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; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1123

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Query Match 38.7%; Score 138.5; DB 6; Length 94;  
Best Local Similarity 46.4%; Pred. No. 2.1e-09;  
Matches 26; Conservative 6; Mismatches 23; Indels 1; Gaps

Qy	4	DACVLP	AVQ	Q	CRG	WE	PR	WAY	S	P	L	L	Q	Q	H	P	F	V	Y	G	G	E	G	N	N	F	H	S	R	E	S	C	B	D	A	C	-	P	V	58										
D6	27	D	I	C	K	L	P	K	E	G	T	C	R	D	F	L	K	W	Y	D	N	T	K	S	C	A	R	F	W	Y	G	G	C	G	N	E	N	F	G	S	O	K	E	K	V	C	A	P	V	82

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RESULT 8
US-11-183-555-5
/ Sequence 5, Application US/11183555
/ Publication No. US20060025329A1
/ GENERAL INFORMATION:
/ APPLICANT: Hambrough, Todd
/ APPLICANT: Papathanasiou, Adonia I
/ APPLICANT: Green, Shawn J
/ TITLE OF INVENTION: Compositions and
/ TITLE OF INVENTION: Comprising TFA
/ FILE REFERENCE: 05213-0297 (43170-
/ CURRENT APPLICATION NUMBER: US/11/
/ CURRENT FILING DATE: 2005-07-18
/ PRIOR APPLICATION NUMBER: US 09/76
/ PRIOR FILING DATE: 2001-01-22
/ PRIOR APPLICATION NUMBER: US 09/22
/ PRIOR FILING DATE: 1999-01-11
/ PRIOR APPLICATION NUMBER: US 08/79
/ PRIOR FILING DATE: 1997-02-06
/ PRIOR APPLICATION NUMBER: US 09/13
/ PRIOR FILING DATE: 1998-08-06
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 5
/ LENGTH: 276
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ US-11-183-555-5

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Query Match 38.5%; Score 138; DB 7; Length 276;  
Best Local Similarity 47.1%; Pred. No. 5.9e-09;  
Matches 24; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

**Qy** 6 CVLPVQGPCRGWEPRWAYSPILQQCHPFVYGGCEGNNFHSRESCDAC 56  
: : : : : : : : : : : : : : : : : :  
**Dh** 189 CTTPADGLCRANENRFYNSVTGKCRPFKYSSCGGNENFYSKOELRAC 239

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RESULT 9
US-10-821-234-1540
/ Sequence 1540, Application US/10821234
/ Publication NO. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 1540
/ LENGTH: 304

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1540

Query Match      38.5%; Score 138; DB 6; Length 304;
Best Local Similarity 47.1%; Pred. No. 6.5e-09;
Matches 24; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Qy 6 CVLPAVGPCRGWPRWAYSPLLQCHPFFVYGGCGGNPNPHSRSCEDAC 56
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 217 CLTPADRGCLCRANENRFYNYSVIGKCRPFKYSGCGGNENFTSKQECILRAC 267

RESULT 10
US-10-821-234-1619
; Sequence 1619, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1619
; LENGTH: 763
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1619

Query Match      37.0%; Score 132.5; DB 6; Length 763;
Best Local Similarity 42.4%; Pred. No. 6e-08;
Matches 25; Conservative 5; Mismatches 24; Indels 5; Gaps 1;

Qy 6 CVLPAVGPCRGWPRWAYSPLLQCHPFFVYGGCGGNPNPHSRSCEDAC-----PVP 59
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 310 CSQEAHTGPCRAVMPRWYFDLSKGCVRFIYGGCGGNRNFFSESDYCMVACKAMIPPTP 368

RESULT 11
US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982.545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503

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; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease
; OTHER INFORMATION: nexin II (FN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(713)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3 (42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3 (40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF (59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF (57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF (50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
US-10-982-545-15

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Query Match 35.8%; Score 128; DB 6; Length 770;

Best Local Similarity 43.4%; Pred. No. 2e-07; Mismatches 4; Indels 0; Gaps 0;  
Matches 23; Conservative 4;

Qy 4 DACVLPVQRCRWEPWYSPYLQOCHPFPVYGGCEGNGNHFHRSCECDAC 56  
Db 289 EVCSEQAETGFCRAMISRWFYDVTGKCAPFFYGGCGNRNRFDTTEYCMVAC 341

## RESULT 12

US-10-789-273-38  
; Sequence 38, Application US/10789273  
; Publication No. US20050249725A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Gurig  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
; FILE REFERENCE: ELM-002CP  
; CURRENT APPLICATION NUMBER: US/10/789,273  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR APPLICATION NUMBER: US/10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 770  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-789-273-38

Query Match 35.8%; Score 128; DB 6; Length 770;

Best Local Similarity 43.4%; Pred. No. 2e-07; Mismatches 4; Indels 0; Gaps 0;  
Matches 23; Conservative 4;

Qy 4 DACVLPVQRCRWEPWYSPYLQOCHPFPVYGGCEGNGNHFHRSCECDAC 56  
Db 289 EVCSEQAETGFCRAMISRWFYDVTGKCAPFFYGGCGNRNRFDTTEYCMVAC 341

## RESULT 13

US-11-068-783-54  
; Sequence 54, Application US/11068783  
; Publication No. US20050260715A1  
; GENERAL INFORMATION:  
; APPLICANT: Burian, Jan  
; APPLICANT: Bartfeld, Daniel  
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING  
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS  
; FILE REFERENCE: 660081.411  
; CURRENT APPLICATION NUMBER: US/11/068,783  
; CURRENT FILING DATE: 2005-02-28  
; PRIOR APPLICATION NUMBER: US/09/444,281  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 54  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Bos taurus  
US-11-068-783-54

Query Match 33.0%; Score 118; DB 7; Length 58;

Best Local Similarity 41.5%; Pred. No. 3e-07; Mismatches 4; Indels 0; Gaps 0;  
Matches 22; Conservative 4;

Qy 4 DACVLPVQRCRWEPWYSPYLQOCHPFPVYGGCEGNGNHFHRSCECDAC 56  
Db 3 DFCLEPPYTGCKARIIRFYFNKAGLCQTFYGGCRKRNNFKSABDCMRTC 55

## RESULT 14

US-11-137-465-44  
; Sequence 44, Application US/11137465  
; Publication No. US20050255558A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdoch, Paul R.  
; APPLICANT: Rizvi, Safia, K.  
; APPLICANT: Smith, Randall, F.  
; APPLICANT: Xiang, Zhaoying  
; APPLICANT: Kabnick, Karen  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50018  
; CURRENT APPLICATION NUMBER: US/11/137,465  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US/10/239,663  
; PRIOR FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: PCT/US01/09226  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 60/192,158  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/192,668  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: 60/200,166  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 44  
; LENGTH: 353  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-137-465-44

Query Match 30.0%; Score 107.5; DB 7; Length 353;

Best Local Similarity 33.1%; Pred. No. 2.2e-05; Mismatches 20; Indels 1; Gaps 1;  
Matches 20; Conservative 10;

Qy 1 GPGDACVLPVQV-GPCRCGWEPWYSPYLQOCHPFPVYGGCEGNGNHFHRSCECDAC 56  
Db 294 GAEDPRCLEALKPGCGEVVRYDYKQVNSCARFWSGCGNSGRNFNSEKQCETC 350

## RESULT 15

US-11-137-465-45  
; Sequence 45, Application US/11137465  
; Publication No. US20050255558A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdoch, Paul R.  
; APPLICANT: Rizvi, Safia, K.  
; APPLICANT: Smith, Randall, F.  
; APPLICANT: Xiang, Zhaoying  
; APPLICANT: Kabnick, Karen  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50018  
; CURRENT APPLICATION NUMBER: US/11/137,465  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US/10/239,663  
; PRIOR FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: PCT/US01/09226  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 60/192,158  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/192,668  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: 60/200,166  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 45  
; LENGTH: 448

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-137-465-45

Query Match 30.0%; Score 107.5; DB 7; Length 448;  
Best Local Similarity 35.1%; Pred. No. 2.7e-05;  
Matches 20; Conservative 10; Mismatches 26; Indels 1; Gaps 1;

Qy 1 GPGDACVLPAVQ-GPCRGNWPRWAYSPLLQQCHPFVYGGCGGNGNFFHRSCEDAC 56  
Db 389 GAEDPRCLEALKPGNGGEYVVRYYDKVNSCARFWFGCGNGSGNRFNSEKECOETC 445

Search completed: February 16, 2006, 18:48:27  
Job time : 17 secs



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